

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 19:41:11 ; Search time 132 seconds

(without alignments)
14615.325 Million cell updates/sec

Title: US-09-918-187-3

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Gapop 60.0 , Gapext 60.0

Searched: 328367 seqs, 184756068 residues

Word size : 0

Total number of hits satisfying chosen parameters: 189310

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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Published Applications_NA:*

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- 12: /cgn2-6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	0.4	22	12	US-10-016-725-4
2	21	0.4	21	12	US-10-016-725-5
3	19	0.4	60	10	US-09-983-965-588
4	19	0.4	63	10	US-09-983-965-323
5	19	0.4	94	10	US-09-783-550-6903
6	19	0.4	98	10	US-09-969-373-1355
7	19	0.4	46	10	US-09-827-289-19
8	18	0.3	46	10	US-09-827-289-23
9	18	0.3	51	10	US-09-983-965-239
10	18	0.3	51	10	US-09-948-018-31
11	18	0.3	51	10	US-09-948-018-32
12	18	0.3	59	10	US-09-783-590-2044
13	18	0.3	64	10	US-09-983-965-5341
14	18	0.3	72	10	US-09-919-580-221
15	18	0.3	72	10	US-09-919-580-343
16	18	0.3	72	10	US-09-923-300-897
17	18	0.3	74	10	US-09-919-580-262
18	18	0.3	74	10	US-09-919-580-394
19	18	0.3	76	10	US-09-969-373-875

C	20	18	0.3	76	10	US-09-983-965-5771	Sequence 5771, App
	21	18	0.3	78	10	US-09-983-965-4261	Sequence 4261, App
	22	18	0.3	79	10	US-09-919-580-206	Sequence 206, App
	23	18	0.3	81	10	US-09-919-580-749	Sequence 749, App
	24	18	0.3	87	10	US-09-783-590-1840	Sequence 1840, App
	25	18	0.3	90	10	US-09-777-564-1230	Sequence 1230, App
	26	18	0.3	90	10	US-09-919-580-157	Sequence 157, App
	27	18	0.3	90	10	US-09-919-580-217	Sequence 217, App
	28	18	0.3	94	10	US-09-969-373-347	Sequence 347, App
	29	18	0.3	97	10	US-09-815-343-241	Sequence 241, App
	30	18	0.3	98	10	US-09-777-564-865	Sequence 865, App
	31	18	0.3	100	10	US-09-867-701-10505	Sequence 10505, App
	32	17	0.3	17	10	US-09-788-362-3	Sequence 3, App1
	33	17	0.3	17	10	US-09-090-6728-106	Sequence 106, App
	34	17	0.3	17	10	US-09-788-383-1	Sequence 3, App1
	35	17	0.3	20	10	US-09-005-243-32	Sequence 32, App1
	36	17	0.3	20	10	US-09-005-243-33	Sequence 33, App1
	37	17	0.3	20	10	US-09-224-683-32	Sequence 32, App1
	38	17	0.3	20	10	US-09-224-683-33	Sequence 33, App1
	39	17	0.3	30	12	US-10-079-616-23	Sequence 23, App1
	40	17	0.3	35	10	US-09-374-671-100	Sequence 100, App1
	41	17	0.3	41	10	US-09-823-648-1	Sequence 1, App1
	42	17	0.3	41	10	US-09-935-592-4	Sequence 4, App1
	43	17	0.3	45	10	US-09-827-289-12	Sequence 12, App1
	44	17	0.3	45	10	US-09-827-289-16	Sequence 16, App1
	45	17	0.3	46	10	US-09-833-498-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-10-016-725-4/c
: Sequence 4, Application US/10016725
: Patent No. US20020151018A1
: GENERAL INFORMATION:
: APPLICANT: Protuity, Stephen
: APPLICANT: Zhang, Lin
: TITLE OF INVENTION: Stearyl-CoA Desaturase Promoter
: FILE REFERENCE: J6J2065
: CURRENT APPLICATION NUMBER: US/10/016,725
: CURRENT FILING DATE: 2002-06-10
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.1
: SEQ. ID NO. 4
: LENGTH: 22
: TYPE: DNA
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: oligonucleotide
US-10-016-725-4

Query Match 0.4%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 70 CGGGACCTCCACGACCGCG 91
22 CGGGACCTCCACGACCGCG 1

RESULT 2
US-10-016-725-6/c
: Sequence 6, Application US/10016725
: Patent No. US20020151018A1
: GENERAL INFORMATION:
: APPLICANT: Protuity, Stephen
: APPLICANT: Zhang, Lin
: APPLICANT: Stenn, Kurt
: TITLE OF INVENTION: Stearyl-CoA Desaturase Promoter
: FILE REFERENCE: J6J2065
: CURRENT APPLICATION NUMBER: US/10/016,725

;; PRIOR FILING DATE: 1999-12-15
;; PRIOR APPLICATION NUMBER: US 60/113,678

;; PRIOR FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 09/760,427
;; PRIOR FILING DATE: 2001-01-13

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; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1355
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1355

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Best Local Similarity 100.0%; Pred. No. 4.6e+02; Length 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2392 AATATATATACATATATA 2410
Db 52 TCTAATATATACATATATA 70

RESULT 7
US-09-827-289-19/c
; Sequence 19, Application US/09827289
; Patent No. US2002009716A1
; GENERAL INFORMATION:
; APPLICANT: Adarva, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-19

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Length 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5204 TCTAAAAAAAAAAAAA 5221
Db 19 TCTAAAAAAAAAAAAA 2

RESULT 8
US-09-827-289-23/c
; Sequence 23, Application US/09827289
; Patent No. US2002009716A1
; GENERAL INFORMATION:
; APPLICANT: Adarva, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
OTHER INFORMATION: use in allele discrimination
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US-09-827-289-23

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Length 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5204 TCTAAAAAAAAAAAAA 5221
Db 19 TCTAAAAAAAAAAAAA 2

RESULT 9
US-09-983-965-239/c
; Sequence 239, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 239
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 29-BOVMS1-021-Q1-E1-H9
US-09-983-965-239

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4501 TTTT TTTT TTTT TTTT GGG 4518
Db 36 TTTT TTTT TTTT TTTT GGG 19

RESULT 10
US-09-948-018-31
; Sequence 31, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 0101737677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 51
; TYPE: DNA
; ORGANISM: primer
US-09-948-018-31

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Length 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 278 ACCACCACCACCACCAT 295
Db 19 ACCACCACCACCACCAT 19
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 18:17:16 ; Search time 660 Seconds

(without alignments)
17814.672 Million cell updates/sec

Title: US-09-918-187-3

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 2389434

Minimum DB seq length: 8

Maximum DB seq length: 100

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	46	0.9	54	17	AAT28167	Sensence-related
c 2	39	0.7	39	17	AAT28105	Probe 10F1 isolate
c 3	25	0.5	51	22	AAU28163	Human SNP oligonuc
c 4	22	0.4	22	21	AAU28173	Reverse PCR primer
c 5	22	0.4	22	24	ABU57449	Human stearyl-CoA
c 6	22	0.4	22	24	ABU57451	Human stearyl-CoA
c 7	21	0.4	54	21	AAU23240	Human secreted pro
c 8	21	0.4	71	24	AAU64195	Labelled probe use
c 9	21	0.4	95	20	AAU03761	Mouse stearyl-CoA

10	21	0.4	95	21	AAA9683	SEQ ID NO: 3 for 1
c 11	20	0.4	25	21	AAU96419	HLA DPA1 gene PCR
c 12	20	0.4	51	22	AAU32243	Human SNP oligonuc
c 13	20	0.4	95	17	AAT13984	Stearyl-CoA desat
c 14	19	0.4	21	16	AAU75709	Reverse transcript
c 15	19	0.4	21	16	AAU75609	Reverse transcript
c 16	19	0.4	28	24	ABU94876	Fat regulated gene
c 17	19	0.4	41	24	ABU40941	Human nucleotide e
c 18	19	0.4	51	22	AAU30447	Human SNP oligonuc
c 19	18	0.3	18	19	AAU54171	Nucleotide sequenc
c 20	18	0.3	18	21	AAU90641	Human adipose tiss
c 21	18	0.3	20	16	AAU75576	Reverse transcript
c 22	18	0.3	20	16	AAU75559	Reverse transcript
c 23	18	0.3	20	16	AAU75707	Reverse transcript
c 24	18	0.3	21	16	AAU75708	Reverse transcript
c 25	18	0.3	21	16	AAU75710	Reverse transcript
c 26	18	0.3	21	16	AAU75607	Reverse transcript
c 27	18	0.3	21	16	AAU75608	Reverse transcript
c 28	18	0.3	21	16	AAU75610	Reverse transcript
c 29	18	0.3	21	21	AAU77065	Human biallelic ma
c 30	18	0.3	23	16	AAU75028	LCR oligo 2. Synt
c 31	18	0.3	23	16	AAU75029	LCR oligo 3. Synt
c 32	18	0.3	24	24	ABU55130	Human gonadotropin
c 33	18	0.3	25	21	AAU57628	Collagen IV alpha
c 34	18	0.3	25	21	AAU248040	Human Alport syndr
c 35	18	0.3	27	20	AAU23569	Deletion sequence
c 36	18	0.3	27	20	AAU23572	Deletion sequence
c 37	18	0.3	29	21	AAU24732	PCR primer GST-B2
c 38	18	0.3	30	22	AAU28326	DNA EDTA probe (1-
c 39	18	0.3	30	22	AAU28309	Target duplex for
c 40	18	0.3	31	16	AAU99580	Human TPO anti-sen
c 41	18	0.3	33	20	AAU56253	Beta-globin amplic
c 42	18	0.3	33	21	AAU93951	NGF-polyt probe us
c 43	18	0.3	34	21	AAU10930	Pseudo-loxp site B
c 44	18	0.3	35	16	AAU87903	Normalised library
c 45	18	0.3	38	18	AAT72973	Linear probe P65 u

ALIGNMENTS

RESULT 1	
AAT28167/c	
ID	AAU28167 standard; DNA: 54 BP.
XX	
AC	AAT28167;
XX	
DT	06-JAN-1997 (first entry)
XX	
DE	Sensence-related gene sequence 10F1.
XX	
KM	Human: fibroblast; AIDS; enhanced differential display; mRNA preparation;
KM	gene expression; quiescent cell; dividing cell; senescence-related gene;
KM	therapy; liver spot; donor tissue; senescent melanocyte; melanin;
KM	hypodermatation; ss.
XX	
OS	Synthetic.
XX	
PN	WO9613610-A2.
XX	
PD	09-MAY-1996.
XX	
PF	24-AUG-1995; 95WO-0511230.
XX	
PR	31-OCT-1994; 94US-0332420.
XX	
PA	(GERO-) GERON CORP.
XX	
PI	Feng J, Funk W, Hirsch KS, Linskens MHK, Villeponteau B;
XX	West MD.
DR	WPI; 1996-251464/25.

XX Identifying, isolating and regulating senescence-related genes -
 PT useful to ameliorate problems associated with accumulation of
 PT senescent cells, e.g. age-related lipofuscin accumulation in the
 PT retina and AIDS

PS Claim 8; Page 51; 135pp: English.

XX
 CC AAT28076-T28113, and AAT28131-T28173 represent novel senescent-related
 CC gene sequences isolated from fibroblasts using the method of the
 CC invention. In the method of the invention, mRNA is isolated from a
 CC senescent cell, and a young quiescent cell, and the mRNAs are amplified
 CC (using primers such as those shown in AAT28044-T28075) in separate
 CC reaction mixtures. The amplified sequences are then separated by size or
 CC charge, and the products are analysed to identify a gene from young
 CC quiescent cells and dividing cells, that is present at a different level
 CC from senescent cells. To enhance the method even more, it can be
 CC performed in conjunction with an enhanced differential display (EDD)
 CC method (an mRNA preparation method) on the fibroblasts. The method can
 CC be used for the rapid and efficient identification and isolation of
 CC senescence-related genes and gene products, and to detect and distinguish
 CC between senescent and non-senescent cells. It can also be used to
 CC destroy cells expressing senescence specific (or related) gene products,
 CC and to screen for compounds capable of altering gene expression in
 CC senescent cells. The method can also be used to ameliorate problems
 CC associated with the accumulation of senescent cells such as age-related
 CC lipofuscin accumulation in the retina, and in the treatment of AIDS.
 CC Also, the method can be used to distinguish young cells from senescent
 CC cells in donor tissue, which is useful in removing senescent melanocytes
 CC overexpressing melanin which cause hypopigmentation, or liver spots.
 CC
 SQ Sequence 54 BP; 17 A; 9 C; 9 G; 19 T; 0 other;

Query Match 0.9%; Score 46; DB 17; Length 54;
 Best Local Similarity 100.0%; Pred. No. 9.7e-08;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1410 AAGATGATGATGTTAACCCATTCACGATGATCTTTAAAT 1455
 DB 46 AAGATGATGATGTTAACCCATTCACGATGATCTTTAAAT 1

RESULT 2
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 ID AAT28105 standard; DNA; 39 BP.
 XX
 AC AAT28105;
 XX
 DT 31-DEC-1996 (first entry)
 XX
 DE Probe 10F1 isolated from fibroblasts.

XX
 KM Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
 KM enhanced differential display; EDD; mRNA preparation; senescent cell;
 KM quiescent cell; dividing cell; senescence-related gene; gene expression;
 KM non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
 KM donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.

OS Synthetic.

XX WO9613610-A2.

XX 09-MAY-1996.

XX 24-AUG-1995; 95WO-US11230.

XX 31-OCT-1994; 94US-0332420.

XX (GERO-) GERON CORP.

XX Feng J, Funk W, Hirsch KS, Linskens MHK, Villeponteau B;
 PI West MD;
 XX

DR WP1; 1996-251464/25.

XX Identifying, isolating and regulating senescence-related genes -
 PT useful to ameliorate problems associated with accumulation of
 PT senescent cells, e.g. age-related lipofuscin accumulation in the
 PT retina and AIDS

PS Claim 8; Page 38; 135pp: English.

XX
 CC AAT28076-T28113, and AAT28131-T28173 represent novel senescent-related
 CC gene sequences isolated from fibroblasts using the method of the
 CC invention. In the method of the invention, mRNA is isolated from a
 CC senescent cell, and a young quiescent cell, and the mRNAs are amplified
 CC (using primers such as those shown in AAT28044-T28075) in separate
 CC reaction mixtures. The amplified sequences are then separated by size or
 CC charge, and the products are analysed to identify a gene from young
 CC quiescent cells and dividing cells, that is present at a different level
 CC from senescent cells. To enhance the method even more, it can be
 CC performed in conjunction with an enhanced differential display (EDD)
 CC method (an mRNA preparation method) on the fibroblasts. The method can
 CC be used for the rapid and efficient identification and isolation of
 CC senescence-related genes and gene products, and to detect and distinguish
 CC between senescent and non-senescent cells. It can also be used to
 CC destroy cells expressing senescence specific (or related) gene products,
 CC and to screen for compounds capable of altering gene expression in
 CC senescent cells. The method can also be used to ameliorate problems
 CC associated with the accumulation of senescent cells such as age-related
 CC lipofuscin accumulation in the retina, and in the treatment of AIDS.
 CC Also, the method can be used to distinguish young cells from senescent
 CC cells in donor tissue, which is useful in removing senescent melanocytes
 CC overexpressing melanin which cause hypopigmentation, or liver spots.
 CC
 SQ Sequence 39 BP; 11 A; 7 C; 6 G; 15 T; 0 other;

Query Match 0.7%; Score 39; DB 17; Length 39;
 Best Local Similarity 100.0%; Pred. No. 4.9e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1412 AGATGATGATGTTAACCCATTCACGATGATCTTTT 1450
 DB 1 AGATGATGATGTTAACCCATTCACGATGATCTTTT 39

RESULT 3
 AAL28163
 ID AAL28163 standard; DNA; 51 BP.
 XX
 AC AAL28163;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #1371.

XX
 KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KM amyloid protein; apoptosis; apoptosis related protein; cadherin;
 KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KM complement related protein; cytochrome; kinase; cytokine; interleukin;
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KM multifactorial disease; autoimmune disease; infection;
 KM nervous system disease; ss.

OS Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI: 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1, Page 1772; 4143pp: English.
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 CC
 XX Sequence 51 BP; 11 A; 18 C; 15 G; 7 T; 0 other;
 XX
 SQ
 Query Match 0.5%; Score 25; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 200 CCCCCTGGAAGTATCCGCGCATC 224
 Db 1 CCCCCTGGAAGTATCCGCGCATC 25
 RESULT 4
 AAZ61573/C
 ID AAZ61573 standard; DNA: 22 BP.
 XX
 AC AAZ61573;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Reverse PCR primer used to amplify skin stearyl-CoA desaturase cDNA.
 XX
 KW Human; skin; stearyl-CoA desaturase; SCD; unsaturated fatty acid;
 KW skin disorder; skin cancer; hypertrichosis; hirsutism; acne;
 KW atopic dermatitis; alopecia; gene therapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PA WO200009754-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 12-AUG-1999; 99WO-US18387.
 XX
 PR 14-AUG-1998; 98US-0096520.
 PR 05-AUG-1999; 99US-0096520.
 XX
 PA (JOHU) JOHNSON & JOHNSON CONSUMER CO INC.
 XX
 PI Stenn K, Prouty SM, Parimoo S, Zhang L;
 XX
 DR WPI: 2000-224373/19.
 PT Novel nucleic acid useful for diagnosing and treating human skin
 PT disorder comprises sequences encoding human stearyl-CoA desaturase

XX
 PS Disclosure; Page 46; 91pp: English.
 XX
 CC PCR primers AAZ61572-73 were used to amplify human skin stearyl-CoA
 CC desaturase (SCD) cDNA sequences. SCD is responsible for the production
 CC of unsaturated fatty acids, which are required for energy and lipid
 CC metabolism, membrane structure and signal transduction. The SCD
 CC polymorphic nucleic acids and polypeptides are useful for diagnosing a skin
 CC disorder by an abnormal level of SCD expression. The polypeptide is
 CC useful for determining whether an agent increases or decreases the
 CC expression level or activity of human SCD in skin cells. Such compounds
 CC are useful for treating human skin disorders such as skin cancer,
 CC hypertrichosis and hirsutism which is characterized by an excess of
 CC SCD activity. The SCD polypeptides and polynucleotides are also useful
 CC for treating human skin disorders such as acne, atopic dermatitis and
 CC alopecia. The SCD polynucleotide is also useful in gene therapy.
 XX
 SQ Sequence 22 BP; 5 A; 8 C; 3 G; 6 T; 0 other;
 XX
 Query Match 0.4%; Score 22; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1,8e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 861 AACTGTCATGTTCCAGAGGAG 882
 Db 22 AACTGTCATGTTCCAGAGGAG 1
 RESULT 5
 ABL57449/C
 ID ABL57449 standard; DNA: 22 BP.
 XX
 AC ABL57449;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human stearyl-CoA desaturase gene antisense PCR primer.
 XX
 KW Stearyl-CoA desaturase; SCD; enzyme; human; promoter; vitruide;
 KW dermatological; cytostatic; immunosuppressive; anti-allergic;
 KW antiarthritic; antiinflammatory; cardiovascular; antineoplastic;
 KW gene therapy; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PA WO200236780-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 31-OCT-2001; 2001WO-US45199.
 XX
 PR 31-OCT-2000; 2000US-244508P.
 PR 30-OCT-2001; 2001US-0244508.
 XX
 PA (JOHU) JOHNSON & JOHNSON CONSUMER CO INC.
 XX
 PI Prouty SM, Zhang L, Stenn KS;
 XX
 DR WPI: 2002-471502/50.
 XX
 PT New human stearyl-CoA desaturase gene promoter, useful for treating a
 PT skin diseases (e.g. acne, psoriasis and rosacea), tumor diseases,
 PT leukemias, autoimmune diseases, allergies, arthritis, inflammations, or
 PT organ rejections -
 XX
 PS Example 2; Page 14; 53pp: English.
 XX
 CC The present sequence is that of a PCR primer that is complementary
 CC to nucleotides -166 to -145 of the human stearyl-CoA desaturase
 CC (SCD) gene (see ABL57445) on chromosome 10. The primer was used as
 CC an antisense primer in the preparation of SCD-luciferase reporter
 CC constructs that were used in the functional analysis of the SCD
 CC promoter. The sense primers are given in ABL57446-48. The present

CC invention provides the human SCD gene promoter and its functional
 CC molecules, fragments and variants, nucleic acid constructs and
 CC vectors that contain such sequences, and their uses. The promoter
 CC may be used for selective transgene expression in various tissues
 CC such as the skin for treating a skin disease (e.g. acne, psoriasis
 CC and rosacea), tumours, leukaemia, autoimmune diseases, allergy,
 CC arthritis, inflammation, organ rejection, graft versus host
 CC reaction, diseases of the blood coagulation system, cardiovascular
 CC diseases, anaemia, infections and damage to the central nervous
 CC system.

XX Sequence 22 BP; 1 A; 8 C; 10 G; 3 T; 0 other;

Query Match 0.4%; Score 22; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGGGACCTCCACGCCGCGG 91

Db 22 CGGGACCTCCACGCCGCGG 1

RESULT 6

ABL57451/C

ID ABL57451 standard; DNA: 21 BP.

XX ABL57451;

DT 22-AUG-2002 (first entry)

XX Human stearyl-CoA desaturase gene antisense PCR primer.

XX Stearyl-CoA desaturase; SCD; enzyme; human; promoter; virucide;

XX dermatological; cytostatic; immunosuppressive; antiallergic;

XX antirheumatic; antiinflammatory; cardiovascular; antianemic;

XX gene therapy; PCR; primer; ss.

XX Homo sapiens.

XX MO200236780-A2.

XX 10-MAY-2002.

XX 31-OCT-2001; 2001WO-US45199.

XX 31-OCT-2000; 2000US-244508P.

XX 30-OCT-2001; 2001US-0244508.

XX (JOHN J. JOHNSON & JOHNSON CONSUMER CO INC.

XX Prouty SM, Zhang L, Steen KS;

XX WPI: 2002-471502/50.

XX New human stearyl-CoA desaturase gene promoter, useful for treating a

XX skin diseases (e.g. acne, psoriasis and rosacea), tumor diseases,

XX leukemias, autoimmune diseases, allergies, arthritis, inflammations, or

XX organ rejections -

XX Example 3; Page 14; 53pp; English.

XX The present sequence is that of an antisense PCR primer corresponding

XX to nucleotides +7 to +27 of the human stearyl-CoA desaturase

XX (SCD) gene (see ABL57445). It was used with the sense primer given

XX in ABL57450 for the PCR amplification of an SCD gene fragment

XX (nucleotides -275 to +27) which was used in an Rnase protection

XX assay to find the SCD transcription initiation site. The present

XX invention provides the human SCD gene promoter and its functional

XX molecules, fragments and variants, nucleic acid constructs and

XX vectors that contain such sequences, and their uses. The promoter

XX may be used for selective transgene expression in various tissues

XX such as the skin for treating a skin disease (e.g. acne, psoriasis

XX and rosacea), tumours, leukaemia, autoimmune diseases, allergy,

CC arthritis, inflammation, organ rejection, graft versus host
 CC reaction, diseases of the blood coagulation system, cardiovascular
 CC diseases, anaemia, infections and damage to the central nervous
 CC system.

XX Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 other;

Query Match 0.4%; Score 21; DB 24; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 GCCCAGCTGCTGCAGACGAT 262

Db 21 GCCCAGCTGCTGCAGACGAT 1

RESULT 7

AAC23240

ID AAC23240 standard; cDNA; 54 BP.

XX AAC23240;

DT 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 27315.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.

XX Claim 1; SEQ ID 27315; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from

XX mRNAs encoding secreted proteins. No ORF has yet been conclusively from

XX identified within the present sequence. The 5 ESTs were prepared from

XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

XX sequences usually correspond mainly to the 3' untranslated region (UTR)

XX of the mRNA because they are often obtained from oligo-dT primed cDNA

XX libraries. Such ESTs are not well suited for isolating cDNA sequences

XX derived from the 5' ends of mRNAs and even in those cases where longer

XX cDNA sequences have been obtained, the full 5' UTR is rarely included.

XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be

XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used

XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX They are used to obtain upstream regulatory sequences and to design

XX expression and secretion vectors.

XX Sequence 54 BP; 1 A; 5 C; 2 G; 46 T; 0 other;

Query Match 0.4%; Score 21; DB 21; Length 54;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2124 TTTCTTTTCTTTTCTTT 2144

```

Db      14 TTTCTTTCTTTCTTTCTTT 34
          |||
RESULT 8
AA164195/C
ID      AA164195 standard; DNA: 71 BP.
XX
XX      AA164195;
XX
XX      18-JUN-2002 (first entry)
XX
XX      Labelled probe used in a telomerase detection/measurement assay.
DE
XX      Telomerase; cancer; cytostatic; antiproliferative; antirheumatic;
KW      antirheumatic; immunosuppressive; procoagulant; fungicide; tumour;
KW      hyperproliferative; autoimmune disorder; psoriasis; soil;
KW      rheumatoid arthritis; infection; anti-cancer agent; plant disease;
KW      flavone; isoflavone; probe; ss.
XX
XX      unidentified.
OS
XX
XX      Key
FH      modified_base
FT      21
FT      /tag- a
FT      /mod_base- OTHER
FT      /note- "OTHER = Phosphorylated"
FT      22..71
FT      /tag- b
FT      /note- "Can be optionally serially deleted from the
FT      3' end"
XX
XX      WO200180855-A1.
XX
XX      01-NOV-2001.
XX
XX      26-APR-2001; 2001WO-US13419.
XX
XX      27-APR-2000; 2000US-200171P.
XX
XX      (GERO-) GERON CORP.
XX
XX      Chin AC, Tolman RL, Gryaznov S, Matray T;
PI      WPI: 2002-026116/03.
DR
XX
XX      Use of substituted flavone or isoflavone compounds for inhibiting
PT      telomerase activity, and treating e.g. cancer
XX
XX      Example 4; Page 32; 46pp; English.
PS
XX      The present sequence is that of a labelled probe used in a telomerase
CC      detection and measurement assay used to test the efficacy of the
CC      compounds of the invention as telomerase inhibitors. The specification
CC      describes a method of inhibiting telomerase activity in a cell,
CC      comprising contacting the cell with a flavone or isoflavone compound. The
CC      invention has cytostatic, antiproliferative, antirheumatic, antitumour,
CC      immunosuppressive, procoagulant and fungicidal activities. The compounds
CC      of the invention act as telomerase inhibitors and are used for treating
CC      telomerase mediated conditions or diseases, e.g. tumours. They may also
CC      be used to treat hyperproliferative or autoimmune disorders, such as
CC      psoriasis, rheumatoid arthritis; immune system disorders requiring immune
CC      system suppression; immune system reactions to poison ivy or poison oak;
CC      also nematode, protozoan and fungal infections. The compounds can be
CC      administered with other active agents, e.g. anti-cancer agents. The
CC      compounds can also be administered to plants and soil infected with
CC      phytopathogenic organisms having telomerase activity, alone or in
CC      combination with other agents to control plant diseases. The compounds
CC      can be used for a wide variety of malignant cell types and are highly
CC      selective, avoiding the problems of current cancer treatments, which are
CC      non-specific and toxic.
XX
XX      Sequence 71 BP; 56 A; 12 C; 0 G; 3 T; 0 other;
SQ

```

```

Query Match      0.4%; Score 21; DB 24; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4501 TTTTCTTTCTTTCTTTCTTTGCGTGA 4521
          |||
Db      36 TTTTCTTTCTTTCTTTGCGTGA 16

RESULT 9
AAK03761
ID      AAK03761 standard; DNA: 95 BP.
XX
XX      AAK03761;
AC
XX      31-MAR-1999 (first entry)
DT
XX      Mouse stearyl-CoA desaturase nucleotide sequence.
DE
XX
XX      Body weight disorder; obesity; appetite regulation; thermoregulation;
KW      anorexia; abnormal food intake; cachexia; thermogenesis; ss.
XX
XX      Mus sp.
OS
XX      US5853975-A.
XX      29-DEC-1998.
PD
XX
XX      26-FEB-1997; 97US-0807861.
PE
XX
XX      26-FEB-1997; 97US-0807861.
PR      26-FEB-1997; 97US-0807861.
PR      23-AUG-1994; 94US-0294522.
PR      06-JUN-1995; 95US-0470868.
PR      23-AUG-1995; 95US-0518878.
XX
XX      (MILL-) MILLENNIUM PHARM INC.
XX
XX      Tartaglia LA;
PI      WPI: 1999-094892/08.
DR
XX
XX      Identifying modulators of C5 protein uncoupling activity - used as
PT      potential regulators of thermogenesis, appetite and body weight,
PT      e.g. for treating obesity, anorexia and cachexia
XX
XX      Disclosure; Fig 3; 83pp; English.
PS
XX
XX      The present invention describes a method for identifying a compound (I)
CC      that modulates C5 protein uncoupling activity by: (a) treating a test
CC      compound with C5 or cells expressing it; (b) measuring the level of
CC      uncoupling activity; and (c) comparing this with level of activity in
CC      the absence of the test compound. Any difference in the levels indicates
CC      a modulator. C5 protein has uncoupling activity, i.e. it can transport
CC      protons across the mitochondrial inner membrane, reducing the proton
CC      motive force and allowing dissipation of caloric energy as heat. It is
CC      thus a regulator of thermogenesis and is involved in body weight
CC      regulation. (I) are potentially useful in treatment of body weight
CC      disorders, regulation of appetite and thermoregulation, e.g. in cases of
CC      obesity, anorexia, abnormal food intake and cachexia. The present
CC      sequence represents a nucleotide sequence from the present invention.
XX
XX      Sequence 95 BP; 24 A; 24 C; 16 G; 31 T; 0 other;
SQ

Query Match      0.4%; Score 21; DB 20; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5069 TTTTCTTTCTTTCTTTCTTTGCGG 5089
          |||
Db      74 TTTTCTTTCTTTCTTTCTTTGCGG 94

```

```

RESULT 10
AAA99683
ID AAA99683 standard; DNA: 95 BP.
XX
AC AAA99683:
XX
DT 06-FEB-2001 (first entry)
XX
DE .SEQ ID NO: 3 for identifying genes associated with body weight disorders.
XX
KW Mouse; body weight; immunomodulator; anorectic; obesity; cachexia;
XX thermogenesis; appetite; ds.
XX
OS Mus sp.
XX
PN US6121017-A.
XX
PD 19-SEP-2000.
XX
PF 08-OCT-1997; 97US-0946719.
XX
PR 26-FEB-1997; 97US-0807861.
PR 23-AUG-1994; 94US-0294522.
PR 06-JUN-1995; 95US-0470868.
PR 23-AUG-1995; 95US-0518878.
XX
PA (MLL-) MILLENNIUM PHARM INC.
XX
PI Tartaglia LA;
XX
DR WPI: 2000-618197/59.
XX
PT New human C5 gene and gene product, useful in regulating mammalian body
PT body weight disorders, e.g. obesity or cachexia -
XX
PS Example: Fig 3B; 84pp; English.
XX
CC The present sequence shows homology to a nucleotide sequence which was
CC found to be differentially expressed in body weight disorder
CC states. The identified sequences may be useful in modulating processes
CC relating to mammalian body weight regulation, including treatment of body
CC weight disorders, e.g. obesity or cachexia, and modulation of
CC thermogenesis. It is also useful in regulating appetite and/or body
CC weight. Furthermore, it is useful for diagnostic evaluation and prognosis
CC of various body weight disorders, and for identifying subjects exhibiting
CC a predisposition to such conditions.
XX
SQ Sequence 95 BP; 24 A; 24 C; 16 G; 31 T; 0 other;
XX
Query Match 0.4%; Score 21; DB 21; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5069 TTTTTCCTTTTATGTGGG 5089
DB 74 TTTTTCCTTTTATGTGGG 94

```

```

OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP03636.
XX
PR 26-APR-1999; 99EP-0303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI: 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences
PT of specific length -
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
XX particular.
XX
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 other;
XX
Query Match 0.4%; Score 20; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5202 AATCTAATAAAAAAAAAA 5221
DB 20 AATCTAATAAAAAAAAAA 1

```

```

RESULT 12
AAL32243/C
ID AAL32243 standard; DNA: 51 BP.
XX
AC AAL32243;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #5451.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cachexin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.

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XX  Shinkets RA, Leach M;
XX
XX  MPI: 2001-465210/50.
XX
XX  Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX  oncogenes and histones, useful for diagnosing and treating, e.g.
XX  cancer, autoimmune diseases and infections -
XX
XX  Claim 1: Page 2956; 4143pp; English.
XX
XX  The present invention relates to oligonucleotides encoding polymorphic
XX  variants of proteins related to amylases, amyloid proteins, angiotensin,
XX  apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX  histones, kinases, colony stimulating factors, complement related
XX  proteins, cytochromes, kinases, cytokines, interferons, interleukins,
XX  G-protein coupled receptors and thioesterases. The present sequence is
XX  one such oligonucleotide. The oligonucleotides and the peptides encoded
XX  by them may be used in the prevention, diagnosis and treatment of
XX  diseases associated with inappropriate expression of the proteins listed
XX  above. Disorders that may be prevented, diagnosed and/or treated include
XX  multifactorial diseases with a genetic component, such as autoimmune
XX  diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX  systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX  (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX  leukaemia), diseases of the nervous system and an infection of pathogenic
XX  organisms.
XX
XX  Sequence 51 BP; 10 A; 2 C; 2 G; 37 T; 0 other;
XX
XX  Query Match      0.4%; Score 20; DB 22; Length 51;
XX  Best Local Similarity 100.0%; Pred. No. 9.7e+02;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY  5202 AACTTAAAAAATAAAAA 5221
XX      |||
XX      30 AACTTAAAAAATAAAAA 11
XX
XX  RESULT 13
XX  AAT13984
XX  AAT13984 standard; cDNA; 95 BP.
XX
XX  AAT13984;
XX
XX  19-JUN-1996 (first entry)
XX
XX  Stearoyl-CoA desaturase gene cDNA clone L36 consensus region.
XX
XX  Obesity; body weight disorder; diagnosis; therapy;
XX  gene modulator; fat; adipose; stearoyl-CoA desaturase; ss.
XX
XX  Mus musculus.
XX
XX  WO9605861-A1.
XX
XX  29-FEB-1996.
XX
XX  23-AUG-1995; 95WO-US10918.
XX
XX  06-JUN-1995; 95US-0470868.
XX  23-AUG-1994; 94US-0294522.
XX
XX  (MILL-) MILLENNIUM PHARM INC.
XX
XX  Tartaglia LA;
XX
XX  MPI: 1996-151150/15.
XX
XX  New gene which is differentially expressed in body weight disorders
XX  - corresp. gene prod., antibodies and gene modulators; for
XX  diagnosing and treating a weight disorder, such as obesity
XX

```

```

PS  Example 6: Fig 3b; 162pp; English.
XX
XX  2 Regions (AAT13983 and AAT13984), complementary to bases 2-157 and
XX  123-217 of mouse cDNA L36 (AAT13982), show marked homology to
XX  nucleotides 3505-3660 and 3447-3541, respectively, of the mouse
XX  stearoyl-CoA desaturase gene SCD1, which encodes an enzyme that
XX  converts saturated fats to mono-unsaturates. L36 cDNA was isolated
XX  using a genetic obesity paradigm for the identification of genes
XX  that are differentially expressed in obese vs. lean mice; levels
XX  of L36 mRNA are higher in livers of obese mice than in livers of
XX  their lean littermates. L36, and other identified genes (see
XX  CC AAT13979-81 and AAT13985-T14008), can be used to diagnose body wt.
XX  disorders.
XX
XX  Sequence 95 BP; 24 A; 26 C; 14 G; 31 T; 0 other;
XX
XX  Query Match      0.4%; Score 20; DB 17; Length 95;
XX  Best Local Similarity 100.0%; Pred. No. 9.2e+02;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY  5069 TTTTTCCTTTTATGCG 5088
XX      |||
XX      76 TTTTTCCTTTTATGCG 95
XX
XX  RESULT 14
XX  AAQ75709/C
XX  AAQ75709 standard; DNA; 21 BP.
XX
XX  AAQ75709;
XX
XX  04-AUG-1995 (first entry)
XX
XX  Reverse transcription primer used in cDNA analysis technique.
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
XX  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
XX
XX  JP06303997-A.
XX
XX  01-NOV-1994.
XX
XX  16-APR-1993; 93JP-0112515.
XX
XX  16-APR-1993; 93JP-0112515.
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX  MPI: 1995-018287/03.
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA
XX  followed by digestion with restriction enzymes
XX
XX  Disclosure: Page 7; 11pp; Japanese.
XX
XX  A method for the analysis of cDNA comprises (a) preparing an
XX  aggregate of double-stranded cDNAs by using an aggregate of mRNAs
XX  and a plural type of labelled reverse transcription primers
XX  (GENESCO files AAO75547-Q75798) and using the aggregate of mRNAs as the
XX  template for each reverse transcription primer; (b) digesting each of
XX  the prepared aggregates of the double-stranded cDNAs with restriction
XX  enzyme and; (c) electrophoresing the digested aggregate of cDNAs in
XX  separate lanes. The method can be used to analyse gene expression
XX  rapidly and easily.
XX
XX  Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 other;
XX
XX  Query Match      0.4%; Score 19; DB 16; Length 21;
XX  Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

```


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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 23:23:31 : Search time 6984 Seconds
(without alignments)
18795.666 Million cell updates/sec

Title: US-09-918-187-3
Perfect score: 5221
Sequence: 1 atctaaaggggcgtgagga.....atctaaaaaaaaaaaaa 5221

Scoring table: OLIGO.MUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13593584

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
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2: /cgn2_6/ptodata/1/pna/US06.COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07.COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08.COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US081.COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US082.COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US083.COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US084.COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US085.COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US086.COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US087.COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US088.COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US089.COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US090.COMB.seq:*
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16: /cgn2_6/ptodata/1/pna/US092.COMB.seq:*
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20: /cgn2_6/ptodata/1/pna/US095A.COMB.seq:*
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23: /cgn2_6/ptodata/1/pna/US096A.COMB.seq:*
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25: /cgn2_6/ptodata/1/pna/US096C.COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US096D.COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096E.COMB.seq:*
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32: /cgn2_6/ptodata/1/pna/US098B.COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098C.COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US099A.COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US099B.COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US099C.COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099D.COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US100A.COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US100B.COMB.seq:*
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41: /cgn2_6/ptodata/1/pna/US101B.COMB.seq:*
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Result No.	Score	Query Match	Length	DB ID	Description
1	98	1.9	98	14	US-09-021-095-3409 Sequence 3409, Ap
2	98	1.9	98	20	US-09-534-845-2201 Sequence 2201, Ap
3	98	1.9	98	20	US-09-534-846-2201 Sequence 2201, Ap
4	88	1.7	88	20	US-09-534-845-2322 Sequence 2322, Ap
5	88	1.7	88	20	US-09-534-846-2322 Sequence 2322, Ap
6	86	1.6	86	12	US-08-839-045-1181 Sequence 1181, Ap
7	86	1.6	86	20	US-09-534-845-2409 Sequence 2409, Ap
8	86	1.6	86	20	US-09-534-846-2409 Sequence 2409, Ap
9	86	1.6	86	45	US-60-015-904-1181 Sequence 1181, Ap
10	86	1.6	86	47	US-60-033-401-570 Sequence 570, Ap
11	81	1.6	81	17	US-09-321-214-13928 Sequence 13928, A
12	81	1.6	81	19	US-09-516-335-19928 Sequence 13928, A
13	81	1.6	81	29	US-09-733-811-13928 Sequence 13928, A
14	81	1.6	81	29	US-09-733-811A-13928 Sequence 13928, A
15	81	1.6	81	36	US-09-975-640-13928 Sequence 13928, A
16	81	1.6	81	36	US-09-975-640A-13928 Sequence 13928, A
17	80	1.5	80	20	US-09-534-845-2135 Sequence 2135, Ap
18	80	1.5	80	20	US-09-534-846-2135 Sequence 2135, Ap
19	77	1.5	77	13	US-08-940-864-94 Sequence 94, Ap1
20	77	1.5	77	20	US-09-534-845-2492 Sequence 2492, Ap
21	77	1.5	77	20	US-09-534-846-2492 Sequence 2492, Ap

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22	77	1.5	77	46	US-60-027-236-94	Sequence 94, Appl
23	51	1.0	51	71	US-60-276-258-1257	Sequence 1257, Ap
24	48	0.9	66	15	US-09-107-910-5087	Sequence 5087, Ap
25	48	0.9	66	20	US-09-534-845-2232	Sequence 2232, Ap
26	48	0.9	66	20	US-09-534-846-2232	Sequence 2232, Ap
27	48	0.9	88	13	US-09-522-303-403	Sequence 403, Ap
28	45	0.9	81	13	US-08-903-474-1413	Sequence 1413, Ap
29	45	0.9	81	20	US-09-534-845-2495	Sequence 2495, Ap
30	45	0.9	81	20	US-09-534-846-2495	Sequence 2495, Ap
31	45	0.9	81	46	US-60-023-339-5377	Sequence 5377, Ap
32	41	0.8	96	17	US-09-342-217-300	Sequence 300, App
33	41	0.8	96	17	US-09-342-217A-300	Sequence 300, App
34	39	0.7	96	34	US-09-912-293-6064	Sequence 6064, Ap
35	39	0.7	39	14	US-09-067-701-62	Sequence 62, Appl
36	35	0.7	88	20	US-09-534-845-2403	Sequence 2403, Ap
37	35	0.7	88	20	US-09-534-846-2403	Sequence 2403, Ap
38	34	0.7	51	71	US-60-278-258-1260	Sequence 1260, Ap
39	34	0.7	85	12	US-08-859-945-1680	Sequence 1680, Ap
40	34	0.7	85	20	US-09-534-845-2292	Sequence 2292, Ap
41	34	0.6	85	20	US-09-534-846-2292	Sequence 2292, Ap
42	29	0.6	94	14	US-09-075-075-1493	Sequence 1493, Ap
43	29	0.6	94	20	US-09-534-845-2490	Sequence 2490, Ap
44	29	0.6	94	20	US-09-534-846-2490	Sequence 2490, Ap
45	28	0.5	72	18	US-09-471-277-3243	Sequence 3243, Ap

ALIGNMENTS

RESULT 1
US-09-021-095-3409
Sequence 3409, Application US/09021095
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: ADRENAL GLAND TUMOR
NUMBER OF SEQUENCES: 3656
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,095
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,210
FILING DATE: February 11, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0318 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 3409:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 98 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 2501485H1
US-09-021-095-3409

Query Match                               1.9%: Score 98; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2918 GAACGTTTCTTCCTTCCTGACAGCAGCCTCCTTGATGATATTCAGAGCAGTAT 2977
|||
DB 1 GAACGTTTCTTCCTTCCTGACAGCAGCCTCCTTGATGATATTCAGAGCAGTAT 60

OY 2978 GACTTGCTGTCGACGAGCAGCTCCCTCTGACAGAGAT 3015
|||
DB 61 GACTTGCTGTCGACGAGCAGCTCCCTCTGACAGAGAT 98

RESULT 2
US-09-534-845-2201
Sequence 2201, Application US/09534845
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
FILE REFERENCE: PD-1001 CIP
CURRENT FILING DATE: 2000-03-24
Prior Application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 24058
SOFTWARE: PERL Program
SEQ ID NO 2201
LENGTH: 98
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu00473404
US-09-534-845-2201

Query Match                               1.9%: Score 98; DB 20; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2918 GAACGTTTCTTCCTTCCTGACAGCAGCCTCCTTGATGATATTCAGAGCAGTAT 2977
|||
DB 1 GAACGTTTCTTCCTTCCTGACAGCAGCCTCCTTGATGATATTCAGAGCAGTAT 60

OY 2978 GACTTGCTGTCGACGAGCAGCTCCCTCTGACAGAGAT 3015
|||
DB 61 GACTTGCTGTCGACGAGCAGCTCCCTCTGACAGAGAT 98

RESULT 3
US-09-534-846-2201
Sequence 2201, Application US/09534846
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
FILE REFERENCE: PD-1001 CIP
FILE REFERENCE: PD-1001 CIP

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;; CURRENT APPLICATION NUMBER: US/09/534,846
;; CURRENT FILING DATE: 2000-03-24
;; Prior application data removed - refer to file wrapper or PALM
;; NUMBER OF SEQ ID NOS: 24058
;; SOFTWARE: PERL Program
;; SEQ ID NO 2201
;; LENGTH: 98
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No: hu00473404
US-09-534-846-2201

Query Match 1.9%; Score 98; DB 20; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2918 GAACGTTTCTCTTCTTCCCTGAGACAGGACCTCTTGTGTATTCAGAGGAGTGTAT 2917
DB 1 GAAGCTTTCTCTTCTTCCCTGAGACAGGACCTCTTGTGTATTCAGAGGAGTGTAT 60

QY 2918 GACTTGCTGTCCAGGAGCTCCCTCTGACACAGAGAT 3015
DB 61 GACTTGCTGTCCAGGAGCTCCCTCTGACACAGAGAT 98

RESULT 4
US-09-534-845-2322
;; Sequence 2322, Application US/09534845
;; GENERAL INFORMATION:
;; APPLICANT: Sellhauer, Jeffrey J.
;; APPLICANT: Delegeane, Angelo M.
;; APPLICANT: Stuart, Susan G.
;; APPLICANT: Stuve, Laura L.
;; APPLICANT: Mullaly, Sara J.
;; APPLICANT: Naughton, Rebecca E.
;; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
;; FILE REFERENCE: PD-1001 CIP
;; CURRENT APPLICATION NUMBER: US/09/534,845
;; CURRENT FILING DATE: 2000-03-24
;; Prior application data removed - refer to PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 24058
;; SOFTWARE: PERL Program
;; SEQ ID NO 2322
;; LENGTH: 88
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No: hu00270005
US-09-534-845-2322

Query Match 1.7%; Score 88; DB 20; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4573 ATCTGGGTATCTCTCTGAAGTAGCTCAATAGTCATCATGAAAGTTAAAAAG 4632
DB 1 ATCTGGGTATCTCTCTGAAGTAGCTCAATAGTCATCATGAAAGTTAAAAAG 60

QY 4633 CGAGTGCCCATGTTATGCTGGTGCTTA 4660
DB 61 CGAGTGCCCATGTTATGCTGGTGCTTA 88

RESULT 5
US-09-534-846-2322
;; Sequence 2322, Application US/09534846
;; GENERAL INFORMATION:
;; APPLICANT: Sellhauer, Jeffrey J.
;; APPLICANT: Delegeane, Angelo M.
;; APPLICANT: Stuart, Susan G.

;; APPLICANT: Stuve, Laura L.
;; APPLICANT: Mullaly, Sara J.
;; APPLICANT: Naughton, Rebecca E.
;; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
;; FILE REFERENCE: PD-1001 CIP
;; CURRENT APPLICATION NUMBER: US/09/534,846
;; CURRENT FILING DATE: 2000-03-24
;; Prior application data removed - refer to file wrapper or PALM
;; NUMBER OF SEQ ID NOS: 24058
;; SOFTWARE: PERL Program
;; SEQ ID NO 2322
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; OTHER INFORMATION: Incyte ID No: hu00270005
US-09-534-846-2322

Query Match 1.7%; Score 88; DB 20; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4573 ATCTGGGTATCTCTCTGAAGTAGCTCAATAGTCATCATGAAAGTTAAAAAG 4632
DB 1 ATCTGGGTATCTCTCTGAAGTAGCTCAATAGTCATCATGAAAGTTAAAAAG 60

QY 4633 CGAGTGCCCATGTTATGCTGGTGCTTA 4660
DB 61 CGAGTGCCCATGTTATGCTGGTGCTTA 88

RESULT 6
US-08-839-045-1181
;; Sequence 1181, Application US/08839045
;; GENERAL INFORMATION:
;; APPLICANT: Gooding, Douglas H.
;; APPLICANT: Stuve, Laura L.
;; APPLICANT: Stuart, Susan G.
;; APPLICANT: Ito, Laura Y.
;; APPLICANT: Akerblom, Ingrid E.
;; APPLICANT: Delegeane, Angelo M.
;; APPLICANT: Naughton, Rebecca E.
;; APPLICANT: Klingler, Tod M.
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
;; TITLE OF INVENTION: NORMAL LUNG AND METASTATIC LUNG CARCINOMA
;; NUMBER OF SEQUENCES: 1831
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/839,045
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/015,904
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LUTHER, BARBARA J.
;; REGISTRATION NUMBER: 33954
;; REFERENCE/DOCKET NUMBER: PD-0158P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 855-0555
;; TELEFAX: (415) 852-0195

; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 1238057
; US-08-839-045-1181

Query Match 1.6%; Score 86; DB 12; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4575 CTTGGGTATTCCTCTGTAAGTGAAGTCAATAGTCAATGAAAGGTTAAAAAGCG 4634
DB 1 CTTGGGTATTCCTCTGTAAGTGAAGTCAATAGTCAATGAAAGGTTAAAAAGCG 60

OY 4635 AGGTGCCATGTATGCTGTGCTTA 4660
DB 61 AGGTGCCATGTATGCTGTGCTTA 86

RESULT 7
US-09-534-845-2409
; Sequence 2409, Application US/09534845

; GENERAL INFORMATION:
; APPLICANT: Sellhameer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Naughton, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
; FILE REFERENCE: PD-1001 CIP
; CURRENT APPLICATION NUMBER: US/09/534,845
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 24058
; SOFTWARE: PERL Program
; SEQ ID NO 2409
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00260157
US-09-534-845-2409

Query Match 1.6%; Score 86; DB 20; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4575 CTTGGGTATTCCTCTGTAAGTGAAGTCAATAGTCAATGAAAGGTTAAAAAGCG 4634
DB 1 CTTGGGTATTCCTCTGTAAGTGAAGTCAATAGTCAATGAAAGGTTAAAAAGCG 60

OY 4635 AGGTGCCATGTATGCTGTGCTTA 4660
DB 61 AGGTGCCATGTATGCTGTGCTTA 86

RESULT 8
US-09-534-846-2409
; Sequence 2409, Application US/09534846

; GENERAL INFORMATION:
; APPLICANT: Sellhameer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Naughton, Sara J.
; APPLICANT: Naughton, Rebecca E.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING OXIDOREDUCTASES
; FILE REFERENCE: PD-1001 CIP
; CURRENT APPLICATION NUMBER: US/09/534,846
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to file wrapper or PALM
; NUMBER OF SEQ ID NOS: 24058
; SOFTWARE: PERL Program
; SEQ ID NO 2409
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00260157
US-09-534-846-2409

Query Match 1.6%; Score 86; DB 20; Length 86;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4575 CTTGGGTATTCCTCTGTAAGTGAAGTCAATAGTCAATGAAAGGTTAAAAAGCG 4634
DB 1 CTTGGGTATTCCTCTGTAAGTGAAGTCAATAGTCAATGAAAGGTTAAAAAGCG 60

OY 4635 AGGTGCCATGTATGCTGTGCTTA 4660
DB 61 AGGTGCCATGTATGCTGTGCTTA 86

RESULT 9
US-60-015-904-1181
; Sequence 1181, Application US/60015904

; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: NORMAL LUNG AND METASTATIC LUNG CARCINOMA
; NUMBER OF SEQUENCES: 1831
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/015,904
; FILING DATE:

CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PD-0158P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 852-0195
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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: MOLECULE TYPE: CDNA
: IMMEDIATE SOURCE:
: CLONE: 1238057
US-60-015-904-1181

Query Match
Best Local Similarity 100.0%; Score 86; DB 45; Length 86;
Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4575 CTTGGGTGATTCCTGTAAGTACGTCACAAATAGTCATCATGAAAGCTTAAAAAGCG 4634
DB 1 CTTGGGTGATTCCTGTAAGTACGTCACAAATAGTCATCATGAAAGCTTAAAAAGCG 60
OY 4635 AGGTGGCCATGTTATGCTGGTGTTA 4660
DB 61 AGGTGGCCATGTTATGCTGGTGTTA 86

RESULT 10
US-60-033-401-570
: Sequence 570, Application US/60033401
: GENERAL INFORMATION:
: APPLICANT: Gooding, Douglas H.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Ito, Laura Y.
: APPLICANT: Akerblom, Ingrid E.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Klingler, Tod M.
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
: TITLE OF INVENTION: NEUROCANGLION TUMOR
: NUMBER OF SEQUENCES: 3552
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/60/033,401
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: GERONE, MICHAEL C.
: REGISTRATION NUMBER: 39,132
: REFERENCE/DOCKET NUMBER: PD-0297P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 855-0555
: TELEFAX: (415) 845-4166
: INFORMATION FOR SEQ ID NO: 570:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 86 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: IMMEDIATE SOURCE:
: CLONE: 2306414H1
US-60-033-401-570

Query Match
Best Local Similarity 100.0%; Score 86; DB 47; Length 86;
Pred. No. 6.2e-15;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4575 CTTGGGTGATTCCTGTAAGTACGTCACAAATAGTCATCATGAAAGCTTAAAAAGCG 4634
|||||
```

```

DB 1 CTTGGGTGATTCCTGTAAGTACGTCACAAATAGTCATCATGAAAGCTTAAAAAGCG 60
OY 4635 AGGTGGCCATGTTATGCTGGTGTTA 4660
DB 61 AGGTGGCCATGTTATGCTGGTGTTA 86

RESULT 11
US-09-321-214-13928
: Sequence 13928, Application US/09321214
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: APPLICANT: Drmanac, Radoje
: APPLICANT: Cirkenjakov, Radomir
: APPLICANT: Dickson, Mark
: APPLICANT: Drmanac, Snezana
: APPLICANT: Labat, Ivan
: APPLICANT: Leshkowitz, Dena
: APPLICANT: Kita, David
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
: FILE REFERENCE: 20411-740
: CURRENT APPLICATION NUMBER: US/09/321,214
: CURRENT FILING DATE: 1999-05-26
: EARLIER FILING DATE: 1998-06-02
: NUMBER OF SEQ ID NOS: 31908
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 13928
: LENGTH: 81
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-321-214-13928

Query Match
Best Local Similarity 100.0%; Score 81; DB 17; Length 81;
Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4434 GCTGCTTTCTTAAAGTCCACATTTGATGAGAGGGGCAAAATTTGAATGATTTTGGAT 4493
DB 1 GCTGCTTTCTTAAAGTCCACATTTGATGAGAGGGGCAAAATTTGAATGATTTTGGAT 60
OY 4494 TTATAGTTTTTTTTTTTTT 4514
DB 61 TTATAGTTTTTTTTTTTTT 81

RESULT 12
US-09-516-335-13928
: Sequence 13928, Application US/09516335
: GENERAL INFORMATION:
: APPLICANT: Alteredbun, Matthew
: APPLICANT: Asghari, Vida
: APPLICANT: Damavandi, Slamin
: APPLICANT: Dickson, Mark
: APPLICANT: Drake, Jim
: APPLICANT: Drmanac, Radoje
: APPLICANT: Engleman, Carlie
: APPLICANT: Faulkner, Brandy
: APPLICANT: Fox, Melvin
: APPLICANT: Garcia, Veronica
: APPLICANT: Giedt, Gretchen
: APPLICANT: Jessen, Aaron
: APPLICANT: Jomek, Leni
: APPLICANT: Jones, Lee
: APPLICANT: Kita, David
: APPLICANT: Labat, Ivan
: APPLICANT: Laroza, Mimi
: APPLICANT: Lomelli, Michelle
: APPLICANT: Nelken, Sarah
: APPLICANT: Nguyen, Kody
: APPLICANT: Nguyen, Lynne
```

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; APPLICANT: Nguyen, Phuong
; APPLICANT: Ngira, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Ralsi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verma, Ron
; APPLICANT: Wachter, Adam
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/516,335
; CURRENT FILING DATE: 2000-03-01
; EARLIER FILING DATE: 1999-05-26
; EARLIER FILING DATE: 1999-05-26
; EARLIER FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-516-335-13928

Query Match      1.6%; Score 81; DB 19; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4434 GCTGCTTTCTTAAGTGGCCACATTGATGAGGGTGAATAATTGATGATTTGAT 4493
DB 1 GCTGCTTTCTTAAGTGGCCACATTGATGAGGGTGAATAATTGATGATTTGAT 60
OY 4494 TTATAGTTTTTTTTTTTTTT 4514
DB 61 TTATAGTTTTTTTTTTTTTT 81

RESULT 13
US-09-733-811-13928
; Sequence 13928, Application US/09733811
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kila, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroza, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Melken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Ngira, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Ralsi, Fariba
```

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; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/733,811
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 60/088,041
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-811-13928

Query Match      1.6%; Score 81; DB 29; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4434 GCTGCTTTCTTAAGTGGCCACATTGATGAGGGTGAATAATTGATGATTTGAT 4493
DB 1 GCTGCTTTCTTAAGTGGCCACATTGATGAGGGTGAATAATTGATGATTTGAT 60
OY 4494 TTATAGTTTTTTTTTTTTTT 4514
DB 61 TTATAGTTTTTTTTTTTTTT 81

RESULT 14
US-09-733-811A-13928
; Sequence 13928, Application US/09733811A
; GENERAL INFORMATION:
; APPLICANT: Hysed, Inc.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Civenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kila, David
; APPLICANT: Ford, John
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-740
; CURRENT APPLICATION NUMBER: US/09/733,811A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/321,214
; PRIOR FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-811A-13928

Query Match      1.6%; Score 81; DB 29; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4434 GCTGCTTTCTTAAGTGGCCACATTGATGAGGGTGAATAATTGATGATTTGAT 4493
DB 1 GCTGCTTTCTTAAGTGGCCACATTGATGAGGGTGAATAATTGATGATTTGAT 60
OY 4494 TTATAGTTTTTTTTTTTTTT 4514
DB 61 TTATAGTTTTTTTTTTTTTT 81
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DB 61 TTATAAGTTTTTTTTTTTTT 81

Job time : 7011 secs

RESULT 15

US-09-975-640-13928

; Sequence 13928, Application US/09975640
; GENERAL INFORMATION:

; APPLICANT: Alterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mini
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjivan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Wachter, Adam
; APPLICANT: Wu, James
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/975,640
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/733,811
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/088,041
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 13928
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-975-640-13928

Query Match 1.6%; Score 81; DB 36; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4434 GCTGCTTTCTTAAGTCCCATTTGAGGAGGGAATTAATTGATGATTTGAT 4493
|||||
DB 1 GCTGCTTTCTTAAGTCCCATTTGATGAGGAGGGAATTAATTGATGATTTGAT 60

OY 4494 TTATAAGTTTTTTTTTTTTT 4514
|||||
DB 61 TTATAAGTTTTTTTTTTTTT 81

Search completed: November 14, 2002, 03:20:06

Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 20:20:34 ; Search time 66 seconds
(without alignments)
13362.707 Million cell updates/sec

Title: US-09-918-187-3

Perfect score: 5221
Sequence: 1 ataaagggggctggagaaa.....aatcctaaaaaaaaaaaaa 5221

Scoring table: OLIGO_MNC

Gapop 60.0, Capext 60.0

Searched: 209617 seqs, 84460702 residues

Word size: 0

Total number of hits satisfying chosen parameters: 282408

Minimum DB seq length: 8

Maximum DB seq length: 100

Post-processing: listing first 45 summaries

Database:

Pending Patents, NA, New:*

- 1: /cgn2_6/prodata/1/pna/US06_NEM.COMB.seq:*
- 2: /cgn2_6/prodata/1/pna/US06_NEM.COMB.seq:*
- 3: /cgn2_6/prodata/1/pna/US07_NEM.COMB.seq:*
- 4: /cgn2_6/prodata/1/pna/US09_NEM.COMB.seq:*
- 5: /cgn2_6/prodata/1/pna/US09_NEM.COMB.seq:*
- 6: /cgn2_6/prodata/1/pna/US10_NEM.COMB.seq:*
- 7: /cgn2_6/prodata/1/pna/US06_NEM.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	0.4	54	5 US-09-513-999C-27315	Sequence 27315, A
2	18	0.3	44	1 PCT-US02-32367-19	Sequence 19, Appl
3	18	0.3	44	6 US-10-267-922-19	Sequence 19, Appl
4	18	0.3	52	5 US-09-513-999C-17952	Sequence 17952, A
5	18	0.3	61	5 US-09-513-999C-27797	Sequence 27797, A
6	18	0.3	67	5 US-09-513-999C-16021	Sequence 16021, A
7	18	0.3	69	5 US-09-513-999C-20419	Sequence 20419, A
8	17	0.3	22	1 PCT-US02-33002-9	Sequence 9, Appl
9	17	0.3	22	1 PCT-US02-33002-18	Sequence 18, Appl
10	17	0.3	56	5 US-09-513-999C-29760	Sequence 29760, A
11	17	0.3	57	5 US-09-513-999C-22073	Sequence 22073, A
12	17	0.3	61	5 US-09-513-999C-18892	Sequence 18892, A
13	17	0.3	61	5 US-09-513-999C-19473	Sequence 19473, A
14	17	0.3	73	5 US-09-513-999C-33156	Sequence 33156, A
15	17	0.3	77	7 US-60-416-172-130	Sequence 130, App
16	17	0.3	84	5 US-09-513-999C-20557	Sequence 20557, A
17	17	0.3	86	5 US-09-513-999C-29018	Sequence 19018, A
18	17	0.3	86	5 US-09-513-999C-19808	Sequence 19808, A
19	17	0.3	87	5 US-09-513-999C-17274	Sequence 17274, A
20	17	0.3	88	5 US-09-513-999C-20729	Sequence 20729, A
21	17	0.3	88	5 US-09-513-999C-27453	Sequence 27453, A
22	17	0.3	89	5 US-09-513-999C-16433	Sequence 16433, A
23	17	0.3	90	5 US-09-513-999C-20579	Sequence 20579, A
24	17	0.3	91	5 US-09-513-999C-14518	Sequence 14518, A
25	17	0.3	91	5 US-09-513-999C-28101	Sequence 28101, A
26	17	0.3	96	5 US-09-513-999C-17469	Sequence 17469, A

27	17	0.3	98	5 US-09-513-999C-23475	Sequence 23475, A
28	17	0.3	98	5 US-09-513-999C-34732	Sequence 34732, A
29	17	0.3	100	5 US-09-513-999C-16076	Sequence 16076, A
30	16	0.3	22	1 PCT-US02-33002-7	Sequence 7, Appl
31	16	0.3	22	1 PCT-US02-33002-8	Sequence 8, Appl
32	16	0.3	22	1 PCT-US02-33002-10	Sequence 10, Appl
33	16	0.3	22	1 PCT-US02-33002-15	Sequence 15, Appl
34	16	0.3	22	1 PCT-US02-33002-16	Sequence 16, Appl
35	16	0.3	22	1 PCT-US02-33002-17	Sequence 17, Appl
36	16	0.3	25	7 US-60-417-190-48907	Sequence 48907, A
37	16	0.3	25	7 US-60-417-190-48908	Sequence 48908, A
38	16	0.3	25	7 US-60-417-190-48909	Sequence 48909, A
39	16	0.3	25	7 US-60-417-190-48910	Sequence 48910, A
40	16	0.3	25	7 US-60-417-190-48911	Sequence 48911, A
41	16	0.3	25	7 US-60-417-190-48912	Sequence 48912, A
42	16	0.3	27	6 US-10-281-513-153	Sequence 153, App
43	16	0.3	32	6 US-10-281-513-245	Sequence 245, App
44	16	0.3	35	5 US-09-518-813R-60	Sequence 60, Appl
45	16	0.3	37	5 US-09-791-190-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-513-999C-27315
: Sequence 27315, Application US/09513999C
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Duclert, A.
: TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
: FILE REFERENCE: 59 US2, REG
: CURRENT FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/122,487
: PRIOR FILING DATE: 1999-02-26
: NUMBER OF SEQ ID NOS: 36681
: SOFTWARE: Patent.pm
: SEQ ID NO: 27315
: LENGTH: 54
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-513-999C-27315

Query Match 0.4%; Score 21; DB 5; Length 54;
Best local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2124 TTTTCTTTCTTTTCTTTCTT 2144
Db 14 TTTTCTTTCTTTTCTTTCTT 34

RESULT 2
PCT-US02-32367-19/c
: Sequence 19, Application PC/TUS0232367
: GENERAL INFORMATION:
: APPLICANT: CHIRON CORPORATION et al.
: TITLE OF INVENTION: IDENTIFICATION OF OLIGONUCLEOTIDES FOR THE CAPTURE,
: FILE REFERENCE: 2301-18346.40 / P18346.005
: CURRENT APPLICATION NUMBER: PCT/US02/32367
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 19
: LENGTH: 44
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:
: OTHER INFORMATION: Oligonucleotide VHRY39

PCT-US02-32367-19

Query Match 0.3%; Score 18; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

OY 4498 AGCTTTTCTTTCTTTT 4515
|||||
DB 24 AACCTTTTCTTTCTTTT 7

RESULT 3

US-10-267-922-19/C
Sequence 19, Application US/10267922
GENERAL INFORMATION:
APPLICANT: SHYAMALA, Venkatakrishna
TITLE OF INVENTION: IDENTIFICATION OF OLIGONUCLEOTIDES FOR THE CAPTURE,
FILE REFERENCE: 2301-18346 / PP18346.004
CURRENT APPLICATION NUMBER: US/10/267,922
CURRENT FILING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 44
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-10-267-922-19

Query Match 0.3%; Score 18; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

OY 4498 AACCTTTTCTTTCTTTT 4515
|||||
DB 24 AACCTTTTCTTTCTTTT 7

RESULT 4

US-09-513-999C-17952/C
Sequence 17952, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 17952
LENGTH: 52
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-17952

Query Match 0.3%; Score 18; DB 5; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

OY 4501 TTTTCTTTTCTTTCTTTTGGG 4518
|||||
DB 51 TTTTCTTTTCTTTCTTTTGGG 34

RESULT 5

US-09-513-999C-27797

Sequence 27797, Application US/09513999C

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 27797
LENGTH: 61
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-27797

Query Match 0.3%; Score 18; DB 5; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

OY 5204 TCTAATAAAAAAAAAAAAAA 5221
|||||
DB 44 TCTAATAAAAAAAAAAAAAA 61

RESULT 6

US-09-513-999C-16021
Sequence 16021, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 16021
LENGTH: 67
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-16021

Query Match 0.3%; Score 18; DB 5; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

OY 5204 TCTAATAAAAAAAAAAAAAA 5221
|||||
DB 46 TCTAATAAAAAAAAAAAAAA 63

RESULT 7

US-09-513-999C-20419
Sequence 20419, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
US-09-513-999C-20419


```

: SEQ ID NO 20419
: LENGTH: 69
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-513-999C-20419

Query Match
Best Local Similarity 100.0%; Score 18; DB 5; Length 69;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5204 TCTAAAAAAAAAAAAA 5221
|||||
Db 49 TCTAAAAAAAAAAAAA 66

RESULT 8
PCT-US02-33002-9/c
: Sequence 9, Application PC/TUS0233002
: GENERAL INFORMATION:
: APPLICANT: Serafini, Tito
: APPLICANT: Chen, Hang
: APPLICANT: Toemmel, Emily
: APPLICANT: Ellis, Michael
: TITLE OF INVENTION: Methods for Nucleic Acid Amplification
: FILE REFERENCE: 2605-1-002PCT
: CURRENT FILING DATE: 2002-10-16
: PRIOR APPLICATION NUMBER: US 10/036,860
: PRIOR FILING DATE: 2001-10-19
: PRIOR APPLICATION NUMBER: US 60/305,666
: PRIOR FILING DATE: 2001-07-16
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 22
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: synthetic sequence
PCT-US02-33002-9

Query Match
Best Local Similarity 0.3%; Score 17; DB 1; Length 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5205 CTAATAAAAAAAAAAA 5221
|||||
Db 22 CTAATAAAAAAAAAAA 6

RESULT 9
PCT-US02-33002-18
: Sequence 18, Application PC/TUS0233002
: GENERAL INFORMATION:
: APPLICANT: Serafini, Tito
: APPLICANT: Chen, Hang
: APPLICANT: Toemmel, Emily
: APPLICANT: Ellis, Michael
: TITLE OF INVENTION: Methods for Nucleic Acid Amplification
: FILE REFERENCE: 2605-1-002PCT
: CURRENT FILING DATE: 2002-10-16
: PRIOR APPLICATION NUMBER: US 10/036,860
: PRIOR FILING DATE: 2001-10-19
: PRIOR APPLICATION NUMBER: US 60/305,666
: PRIOR FILING DATE: 2001-07-16
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 18
: LENGTH: 22
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:

```

```

: OTHER INFORMATION: synthetic sequence
PCT-US02-33002-18

Query Match          0.3%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4501 TTTTTTTTTTTTTTGG 4517
DB 6 TTTTTTTTTTTTTTTGG 22

RESULT 10
US-09-513-999C-29760
: Sequence 29760, Application US/09513999C
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Ductert, A.
: TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
: FILE REFERENCE: 59.US.2.REG
: CURRENT APPLICATION NUMBER: US/09/513,999C
: PRIOR FILING DATE: 2000-02-24
: NUMBER OF SEQ ID NOS: 1999-02-26
: SOFTWARE: Patent.pm
: SEQ ID NO 29760
: LENGTH: 56
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-513-999C-29760

Query Match          0.3%; Score 17; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 6,6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5205 CTAACAAAAAAGAAAAA 5221
DB 38 CTAACAAAAAAGAAAAA 54

RESULT 11
US-09-513-999C-22073
: Sequence 22073, Application US/09513999C
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Ductert, A.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
: FILE REFERENCE: 59.US.2.REG
: CURRENT APPLICATION NUMBER: US/09/513,999C
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/122,487
: PRIOR FILING DATE: 1999-02-26
: NUMBER OF SEQ ID NOS: 36681
: SOFTWARE: Patent.pm
: SEQ ID NO 22073
: LENGTH: 57
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-513-999C-22073

Query Match          0.3%; Score 17; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 6,6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5205 CTAACAAAAAAGAAAAA 5221
DB 41 CTAACAAAAAAGAAAAA 57

RESULT 12

```

```

US-09-513-999C-18892/C
; Sequence 18892, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18892
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-18892

```

```

Query Match
Best Local Similarity 100.0%; Score 17; DB 5; Length 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4501 TTTTCTTTCTTTCTTTTGG 4517
|
Db 56 TTTTCTTTCTTTCTTTTGG 40

```

```

RESULT 13
US-09-513-999C-19473
; Sequence 19473, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 19473
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-19473

```

```

Query Match
Best Local Similarity 100.0%; Score 17; DB 5; Length 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2124 TTTTCTTTCTTTCTTTT 2140
|
Db 38 TTTTCTTTCTTTCTTTT 54

```

```

RESULT 14
US-09-513-999C-33156
; Sequence 33156, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681

```

```

; SOFTWARE: Patent.pm
; SEQ ID NO 33156
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-33156

```

```

Query Match
Best Local Similarity 100.0%; Score 17; DB 5; Length 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4499 AGTTTCTTTCTTTCTTTT 4515
|
Db 52 AGTTTCTTTCTTTCTTTT 68

```

```

RESULT 15
US-60-416-172-130
; Sequence 130, Application US/60416172
; GENERAL INFORMATION:
; APPLICANT: Chang, Hwai Wen
; APPLICANT: Felts, Katherine A.
; APPLICANT: Warren, Amy J.
; APPLICANT: Cooper, Judith R.
; TITLE OF INVENTION: Genes from Human Cancer Cells and Human Tumors
; FILE REFERENCE: 216019-153
; CURRENT APPLICATION NUMBER: US/60/416,172
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: Patent version 3.1
; SEQ ID NO 130
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic primer (cDNA an
; NAME/KEY: misc_feature
; LOCATION: (1)-(11)
; OTHER INFORMATION: Base 1 is a diotinylated guanosine residue
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (75)-(75)
; OTHER INFORMATION: V stands for A, C or G
; NAME/KEY: misc_feature
; LOCATION: (76)-(77)
; OTHER INFORMATION: N stands for A, C, G or T
US-60-416-172-130

```

```

Query Match
Best Local Similarity 100.0%; Score 17; DB 7; Length 77;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4499 AGTTTCTTTCTTTCTTTT 4515
|
Db 55 AGTTTCTTTCTTTCTTTT 71

```

```

Search completed: November 14, 2002, 01:20:47
Job time : 70 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 01:16:55 : Search time 4418 Seconds

(without alignments)
19139.121 Million cell updates/sec

Title: US-09-918-187-3

Perfect score: 5221
Sequence: 1 ataaagggggcgtgagga.....aattctaaaaaaaaaaaaa 5221

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 segs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 357786

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbun:*
3: em_estlin:*
4: em_estlun:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	1.7	91	10	BE546379 601071061
2	73	1.4	73	12	BG113100 602283756
3	58	1.1	100	12	BE695455 MRI-BT079
4	50	1.0	50	9	AU103573 AU103573
5	50	1.0	50	9	AU103578 AU103578
6	47	0.9	50	9	AU103571 AU103571

7	43	0.8	74	12	BG255827	BG255827 602368138
8	42	0.8	42	13	BI223563	BI222563 602941991
9	40	0.8	68	9	AA501922	AA501922 ng54d08.s
10	32	0.6	32	13	BI259338	BI259338 602972590
11	28	0.5	50	9	AU103576	AU103576 AU103576
12	26	0.5	50	9	AU103570	AU103570 AU103570
13	24	0.5	50	9	AU103572	AU103572 AU103572
14	24	0.5	92	9	AA544229	AA544229 v363d12.r
15	22	0.4	68	12	BE357444	BE357444 601653588
16	21	0.4	58	12	BG244918	BG244918 602358371
17	21	0.4	66	17	AZ373877	AZ373877 IM0126005
18	21	0.4	73	9	AI223491	AI223491 qx27c06.x
19	21	0.4	94	9	AI139479	AI139479 q116d01.x
20	21	0.4	97	17	AZ431988	AZ431988 IM0217N07
21	20	0.4	37	2	HS0001541	HS0001541
22	20	0.4	37	10	AV947979	AV947979 Homo sapi
23	20	0.4	38	10	AV739303	AV739303 AV739303
24	20	0.4	38	17	AZ345865	AZ345865 IM0080015
25	20	0.4	39	10	AV949716	AV949716 AV949716
26	20	0.4	42	17	AZ625468	AZ625468 IM0464N22
27	20	0.4	47	10	AV948822	AV948822 AV948822
28	20	0.4	50	17	AZ657819	AZ657819 IM0534E17
29	20	0.4	50	17	AL771848	AL771848 Arabidops
30	20	0.4	52	9	AA611743	AA611743 v089h05.r
31	20	0.4	52	10	AA103102	AA103102 xg43e05.x
32	20	0.4	53	9	AA528632	AA528632 pf02f07.s
33	20	0.4	54	10	AA695135	AA695135 NF091F01S
34	20	0.4	56	9	AI401100	AI401100 fh22d05.x
35	20	0.4	56	14	T25677	T25677 EST00547 Eq
36	20	0.4	58	9	AU264276	AU264276 AU264276
37	20	0.4	58	14	BO385703	BO385703 NISC_mn13
38	20	0.4	59	14	BO614971	BO614971 fab20G05.
39	20	0.4	61	2	HS0001540	HS0001540 Homo sapi
40	20	0.4	61	9	AI630615	AI630615 ad13c06.x
41	20	0.4	63	2	HS0001534	HS0001534 Homo sapi
42	20	0.4	63	12	BG798286	BG798286 Lc07e08.y
43	20	0.4	64	2	HS0001522	HS0001522 Homo sapi
44	20	0.4	67	9	AI348943	AI348943 cb60a11.x
45	20	0.4	68	13	BMS31526	BMS31526 fx88b07.y

ALIGNMENTS

RESULT 1
LOCUS BE546379 91 bp mRNA linear EST 09-AUG-2000
DEFINITION 601071061F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:345723 5',
mRNA sequence.
ACCESSION BE546379
VERSION BE546379.1 GI:9775024
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
http://image.jh1.gov
Plate: LRAM8446 row: 1 column: 16
High quality sequence stop: 91.
Location/Qualifiers
1..91

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3457239"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT 22 a 24 c 26 g 19 t

ORIGIN

Query Match 1.7%; Score 88; DB 10; Length 91;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3230 GTTGAGCCATGGCCAGCAGCAGCAAGAGGCTTTATTTGAGTCCCTCTCTG 3289
|||||
Db 4 GTTGAGCCATGGCCAGCAGCAGCAAGAGGCTTTATTTGAGTCCCTCTCTG 63
|||||

QY 3230 GGTGAGACAGAGGCGATGCTGAATGC 3317
|||||
Db 64 GGTGAGACAGAGGCGATGCTGAATGC 91
|||||

RESULT 2
BG113100

LOCUS BG113100 73 bp mRNA linear EST 30-JAN-2001
DEFINITION 602283756F1 NIH_MGC_86 Homo sapiens cDNA IMAGE:4371325 5',
mRNA sequence.
BG113100
VERSION BG113100.1 GI:12606606
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 73)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gga@bbs.fda.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LHAM10029 row: p column: 14
High quality sequence stop: 73.

FEATURES
source

1..73
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4371325"
/clone_lib="NIH_MGC_86"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full length clones and constructed by Life Technologies.
Note: This is a NIH_MGC Library."
BASE COUNT 12 a 20 c 19 g 22 t
ORIGIN

Query Match 1.4%; Score 73; DB 12; Length 73;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3263 GGGTTATTTTCACTCCCTCTCTGCTGACAGACAGGCGATGCTGAATGCCCT 3322
|||||

Db 1 GGGTTATTTTCACTCCCTCTCTGCTGACAGACAGGCGATGCTGAATGCCCT 60
|||||

QY 3323 GCTTACTTTGGTGA 3335
|||||
Db 61 GCTTACTTTGGTGA 73
|||||

RESULT 3
BE695455

LOCUS BE695455 100 bp mRNA linear EST 11-SEP-2000
DEFINITION M11-BT0796-160600-001-c10 BT0796 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE695455
VERSION BE695455.1 GI:10082615
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 100)
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6tz-M11-BT0796-160>)
600-001-c106t3-2000-06-166t4-1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 100.

FEATURES
source

1..100
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0796"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 24 a 30 c 23 g 23 t
ORIGIN

Query Match 1.1%; Score 58; DB 12; Length 100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1226 GGTCTGCTATGACCGAAGAAAGCTCCAGCCGATCTTGCCAGAGATTAA 1283
|||||

Db 43 GGTCTGCTATGACCGAAGAAAGCTCCAGCCGATCTTGCCAGAGATTAA 100
|||||

RESULT 4
A0103573

LOCUS AU103573 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU103573 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP13102, mRNA sequence.
ACCESSION AU103573
VERSION AU103573.1 GI:13553094
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,I., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"
Location/Qualifiers

BASE COUNT 8 a 18 c 12 g 12 t

ORIGIN

Query Match 1.0%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ACCGTCACCGCTGCGACCTAGACCTTAATTCGCCGCTCGGACCT 78
|||||
1 ACGGTCACCGCTGCGACCTAGACCTTAATTCGCCGCTCGGACCT 50

RESULT 5
LOCUS AU103578 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU103578 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSE01417, mRNA sequence.
ACCESSION AU103578
VERSION AU103578.1 GI:13553099
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,I., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and

FEATURES a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="ADSE01417"
/clone.lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"
Location/Qualifiers

BASE COUNT 10 a 19 c 17 g 4 t

ORIGIN

Query Match 1.0%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 ACCGGGCTAGCGCGACACGAGCTAGCGTCAAGCGCGCGCTCAG 134
|||||
1 ACGCGGCTAGCGCGACACGAGCTAGCGTCAAGCGCGCGCTCAG 50

RESULT 6
LOCUS AU103571 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU103571 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP07904, mRNA sequence.
ACCESSION AU103571
VERSION AU103571.1 GI:13553092
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,I., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="HEP07904"
/clone.lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylflumarate treated U937 cells"
Location/Qualifiers

BASE COUNT 9 a 19 c 17 g 5 t

ORIGIN

Query Match 0.9%; Score 47; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 GCACCGCGGCTAGCGCGACACGAGCTAGCGTCAAGCGCGCGG 129
|||||
1 GCACCGCGGCTAGCGCGACACGAGCTAGCGTCAAGCGCGCGG 47

RESULT 7
LOCUS BG255827 74 bp mRNA linear EST 13-FEB-2001
DEFINITION BG255827 602368138F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4476417 5',

ACCESSION	mRNA sequence.
VERSION	BG255827
KEYWORDS	BG255827.1 GI:12765643
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	NH-MGC http://mgc.ncl.nih.gov/.
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at: http://image.jnl.gov Place: LMAN10303 row: k column: 10 High quality sequence stop: 41.
FEATURES	
SOURCE	Location/Qualifiers 1..74 /organism="Homo sapiens" /db_xref="taxon:9606" /clone IMAGE:4476417" /clone_1lb="NH_MGC_91" /tissue_type="adenocarcinoma, cell_line" /lab_host="DH10B (phage-resistant)" /note="Organ: prostate; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NH_MGC library."
BASE COUNT	11 a 14 c 24 g 25 t
ORIGIN	
Query Match	0.8%; Score 43; DB 12; Length 74;
Best Local Similarity	100.0%; Pred. NO. 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy 2283 CCATCTTCAGCATATTGGTTCCCTCCCATATGTAAATGATG 2325	
Dd 1 CCATCTTCAGCATATTGGTTCTCCCTCATATGTAATAAGATG 43	
RESULT 8	
BI223563	42 bp mRNA linear EST 11-JUL-2001
LOCUS	602941991F1 NTR_MGC_12 Homo sapiens CDNA clone IMAGE:5104919 5',
DEFINITION	mRNA sequence.
ACCESSION	BI223563
KEYWORDS	BI223563.1 GI:14677007
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	NH-MGC http://mgc.ncl.nih.gov/.
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at: http://image.jnl.gov

	Ptace:	LlAM11253	row:	F	column:	24
		High quality sequence stop: 42.				
FEATURES		Location/Qualifiers				
		1..42				
SOURCE		/organism="Homo sapiens"				
		/db_xref="taxon:9606"				
		/clone_image="5104919"				
		/clone_lib="NIH_MGC_12"				
		/tisue_type="cervical carcinoma cell line"				
		/lab_host="DHIOB"				
		/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;				
		Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.				
		Average insert size 1.4 kb. library prepared by Life Technologies."				
BASE COUNT		10 a	11 c	12 g	9 t	
ORIGIN						
	Query Match	0.8%	Score 42;	DB 13;	Length 42;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
MATCHES	42;	Conservative	0;	Mismatches	0;	Gaps 0;
OY	3394 AGAACGAGGGCGATCCGTCAATGCCCTCCTTGACTTCGAGA	3335				
Dn	1 AGAACGAGGGCATGCTCATATCCCCTCCTTGACTTGCTGA	42				
RESULT 9	AA501922	68 bp	mRNA	linear	EST 18-AUG-1997	
LOCUS	ng54d08.s1 NCI_CGAP_L12 Homo sapiens CDNA clone IMAGE:938607,	mrna				
DEFINITION	sequence.					
ACCESSION	AA501922					
VERSION	AA501922.1	GI:2236889				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 68)					
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/cigap.					
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),					
JOURNAL	Tumor Gene Index					
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgabs@email.nhl.gov Tissue procurement: David E. Kleiner, M.D., Ph.D., Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://bio.lnl.gov/dbip/image/image.html Insert Length: 607 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amershams High quality sequence stop: 51. Location/Qualifiers					
FEATURES		1..68				
SOURCE		/organism="Homo sapiens"				
		/db_xref="taxon:9606"				
		/clone_image="938607"				
		/clone_lib="NCI_CGAP_L12"				
		/sex="male"				
		/tisue_type="liver"				
		/lab_host="DHIOB"				
		/note="Vector: PAMP10; mRNA made from invasive hepatocellular carcinoma, CDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."				
BASE COUNT		12 a	20 c	17 g	19 t	
ORIGIN						

Query Match 0.8%; Score 40; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2972 AGTGATGACTGCTGTCACGAGCTCCCTCGACACA 3011
|||||
DB 29 AGTGATGACTGCTGTCACGAGCTCCCTCGACACA 68

RESULT 10
B1259338 32 bp mRNA linear EST 17-JUL-2001
LOCUS 60297250F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5111783 5',
DEFINITION mRNA sequence.
B1259338
ACCESSION B1259338.1 GI:14816575
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 32)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1271 row: d column: 24
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Homo sapiens"
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/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NotI:
Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."

BASE COUNT 5 a 9 g 9 t
ORIGIN

Query Match 0.6%; Score 32; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3304 GGCATGCTGAATGCCCTCTACTTGATGA 3335
|||||
DB 1 GGCATGCTGAATGCCCTCTACTTGATGA 32

RESULT 11
AUI03576 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI03576 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP21416, mRNA sequence.
AUI03576
ACCESSION AUI03576
VERSION AUI03576.1 GI:13553097
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)

AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HEP21416"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 8 a 19 c 14 g 9 t

ORIGIN

Query Match 0.5%; Score 28; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCTTTAAATTCGCGCTCGGGGACT 78
|||||
DB 1 AGCCTTTAAATTCGCGCTCGGGGACT 28

RESULT 12
AUI03570 50 bp mRNA linear EST 30-AUG-2001
LOCUS AUI03570 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP2242, mRNA sequence.
AUI03570
ACCESSION AUI03570
VERSION AUI03570.1 GI:13553091
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HEP2242"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 11 a 11 c 19 g 9 t

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAAAGGGGCTGAGNAATACCGG 26
|||||
Db 25 ATAAAGGGGCTGAGNAATACCGG 50

RESULT 13
AUI03572          50 bp  mRNA  linear  EST 30-AUG-2001
LOCUS            AUI03572 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION      HEP12765, mRNA sequence.
ACCESSION      AUI03572
VERSION        AUI03572.1 GI:13553093
KEYWORDS
SOURCE
ORGANISM        human.
                Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS        Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
                ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
                ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
                Diverse transcriptional initiation revealed by fine, large-scale
                mapping of mRNA start sites
JOURNAL        EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE        21270072
COMMENT        Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: yuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Toshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
                ,S. Construction and characterization of a full length-enriched and
                a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="HEP12765"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"
BASE COUNT      8 a 16 c 12 g 14 t

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ACGGTACCCGTTGCCAGCTCTAG 52
|||||
Db 1 ACGGTACCCGTTGCCAGCTCTAG 24

RESULT 14
AA544229          92 bp  mRNA  linear  EST 01-AUG-1997
LOCUS            AA544229 v163d12.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA
DEFINITION      clone IMAGE:933719 5' similar to gb:S7678 HETEROGENEOUS NUCLEAR
                RIBONUCLEOPROTEIN K (HUMAN);, mRNA sequence.
ACCESSION      AA544229
VERSION        AA544229.1 GI:2292706
KEYWORDS
SOURCE
ORGANISM        house mouse.
                Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 92)
AUTHORS        Maitra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

```

```

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Therling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Maitra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watsn.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:536639.

FEATURES
source
1..92
/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
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/clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="Blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally from mRNA prepared
from 800 blastocysts. Primer: SalI(drf):
5'-CGGTGACCGTGCACCGTCTTTTCTTTT-3'. CDNAs were
cloned into the NotI/SalI sites of a pSPORT vector (Life
Technologies). Two different size selections: B1 (larger
inserts) and B3."
BASE COUNT      51 a 5 c 10 g 26 t

Query Match          0.5%; Score 24; DB 9; Length 92;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5198 AGTGAATCTTAAAAAATAAAAAA 5221
|||||
Db 55 AGTGAATCTTAAAAAATAAAAAA 78

RESULT 15
BP957444          68 bp  mRNA  linear  EST 14-DEC-2000
LOCUS            BP957444 60165358BR2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3836701 3',
DEFINITION      mRNA sequence.
ACCESSION      BP957444
VERSION        BP957444.2 GI:11773914
KEYWORDS
SOURCE
ORGANISM        human.
                Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 68)
AUTHORS        NIH-MGC http://mgc.ncl.nih.gov/
                National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
                On Oct 3, 2000 this sequence version replaced gi:10568253.
                Contact: Robert Strausberg, Ph.D.
                Email: cga@bbs-riemail.nih.gov
                Tissue Procurement: ATCC
                cDNA library Preparation: CLONETECH Laboratories, Inc.
                cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNL at:
                http://image.llnl.gov
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                High quality sequence stop: 52.

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 01:13:16 : Search time 8670 Seconds

(without alignments)
17525.461 Million cell updates/sec

Title: US-09-918-187-3

Perfect score: 5221
Sequence: 1 ataaagggggctgagga.....aatctaaaaaaaaaaaaa 5221

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 993650

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : GenBank:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_tam:*
37: em_htg_vrl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	0.7	39	6 AR003340	AR003340 Sequence
2	21	0.4	95	6 AR002350	AR002350 Sequence
3	21	0.4	95	6 AR030853	AR030853 Sequence
4	21	0.4	95	6 AR068248	AR068248 Sequence
5	21	0.4	95	6 186799	186799 Sequence 3
6	20	0.4	25	6 AX043282	AX043282 Sequence
7	20	0.4	91	3 DDICTINBA	M25215 Dictyostell
8	20	0.4	94	11 G73641	G73641 RZ696F etlo
9	19	0.4	28	6 AX431447	AX431447 Sequence
10	19	0.4	65	6 AX484032	AX484032 Sequence
11	18	0.3	18	6 E32451	E32451 Mammal-der1
12	18	0.3	35	6 AR051500	AR051500 Sequence
13	18	0.3	35	6 116948	116948 Sequence 17
14	18	0.3	35	6 145742	145742 Sequence 17
15	18	0.3	42	6 AR184440	AR184440 Sequence
16	18	0.3	42	6 AX354550	AX354550 Sequence
17	18	0.3	42	6 AX428578	AX428578 Sequence
18	18	0.3	45	6 AX235169	AX235169 Sequence
19	18	0.3	46	6 AX287576	AX287576 Sequence
20	18	0.3	46	6 AX287580	AX287580 Sequence
21	18	0.3	51	6 AX158375	AX158375 Sequence
22	18	0.3	51	6 AX158377	AX158377 Sequence
23	18	0.3	51	6 AX398977	AX398977 Sequence
24	18	0.3	51	6 AX398978	AX398978 Sequence
25	18	0.3	62	6 AX12493	AX12493 Polydengyia
26	18	0.3	65	6 AX485279	AX485279 Sequence
27	18	0.3	71	3 AF177248	AF177248 Bodo salt
28	18	0.3	72	6 AX381283	AX381283 Sequence
29	18	0.3	72	6 AX381405	AX381405 Sequence
30	18	0.3	74	6 AX203346	AX203346 Sequence
31	18	0.3	74	6 AX381324	AX381324 Sequence
32	18	0.3	74	6 AX381456	AX381456 Sequence
33	18	0.3	79	6 AX381268	AX381268 Sequence
34	18	0.3	81	6 AX381811	AX381811 Sequence
35	18	0.3	83	10 MMARAK007	Y58263 Mouse micro
36	18	0.3	89	9 HUMPODK02	D17700 Human gene
37	18	0.3	90	6 AX198863	AX198863 Sequence
38	18	0.3	90	6 AX209390	AX209390 Sequence
39	18	0.3	90	6 AX381219	AX381219 Sequence
40	18	0.3	90	6 AX381279	AX381279 Sequence
41	18	0.3	97	6 AX260590	AX260590 Sequence
42	18	0.3	98	6 AX198479	AX198479 Sequence
43	18	0.3	98	6 AX209025	AX209025 Sequence
44	17	0.3	17	6 BD011732	BD011732 795, a no
45	17	0.3	17	6 E34260	E34260 Polinosis-

ALIGNMENTS

RESULT 1
LOCUS AR003340 39 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 62 from patent US 5744300.
ACCESSION AR003340
VERSION AR003340.1 GI:3964599
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and West,M.David.
TITLE Methods and reagents for the identification and regulation of senescence-related genes

JOURNAL Patent: US 5744300-A 62-28-APR-1998;
FEATURES Location/Qualifiers

source 1..39

BASE COUNT 11 a 7 c 6 g 15 t
ORIGIN

Query Match 0.7%; Score 39; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1-1c-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1412 AGATGATGATGTTAACCCATTCAGTACGATTCCTTT 1450
|||||

Db 1 AGATGATGATGTTAACCCATTCAGTACGATTCCTTT 39

RESULT 2
AR002350 95 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 3 from patent US 5741666.
ACCESSION AR002350
VERSION AR002350.1 GI:3963904
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Compositions and methods, for the treatment of body weight disorders, including obesity
JOURNAL Patent: US 5741666-A 3-21-APR-1998;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGGG 5089
|||||

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 3
AR030853 95 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 3 from patent US 5861485.
ACCESSION AR030853
VERSION AR030853.1 GI:5944067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Polypeptides involved in body weight disorders, including obesity
JOURNAL Patent: US 5861485-A 3-19-JAN-1999;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGGG 5089
|||||

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 4
AR068248 95 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 3 from patent US 5833975.
ACCESSION AR068248
VERSION AR068248.1 GI:6000455
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Methods for identifying compositions for the treatment of body weight disorders, including obesity
JOURNAL Patent: US 5833975-A 3-29-DEC-1998;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGGG 5089
|||||

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 5
I86799 95 bp DNA linear PAT 10-JUN-1998
LOCUS
DEFINITION Sequence 3 from patent US 5702902.
ACCESSION I86799
VERSION I86799.1 GI:3206517
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 95)
AUTHORS Tartaglia,L.Anthony.
TITLE Methods for the diagnosis of body weight disorders including obesity
JOURNAL Patent: US 5702902-A 3-30-DEC-1997;
FEATURES Location/Qualifiers
source 1..95

BASE COUNT 24 a 24 c 16 g 31 t

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGGG 5089
|||||

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 6
AX043282 25 bp DNA linear PAT 23-NOV-2000
LOCUS
DEFINITION Sequence 848 from patent W00065088.
ACCESSION AX043282
VERSION AX043282.1 GI:11341890
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 25)

BASE COUNT 24 a 24 c 16 g 31 t

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGGG 5089
|||||

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 7
AX043282 25 bp DNA linear PAT 23-NOV-2000
LOCUS
DEFINITION Sequence 848 from patent W00065088.
ACCESSION AX043282
VERSION AX043282.1 GI:11341890
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 25)

BASE COUNT 24 a 24 c 16 g 31 t

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGGG 5089
|||||

Db 74 TTTTTCCTTTTATGTGGG 94

RESULT 8
AX043282 25 bp DNA linear PAT 23-NOV-2000
LOCUS
DEFINITION Sequence 848 from patent W00065088.
ACCESSION AX043282
VERSION AX043282.1 GI:11341890
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 25)

BASE COUNT 24 a 24 c 16 g 31 t

Query Match 0.4%; Score 21; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5069 TTTTTCCTTTTATGTGGG 5089
|||||

Db 74 TTTTTCCTTTTATGTGGG 94

AUTHORS Ulfendahl, P.J. and Wong, K.C.
 TITLE Primers for identifying typing or classifying nucleic acids
 JOURNAL Patent: WO 0065088-A 846 02-NOV-2000;
 Marsham Pharmacia Biotech AB (SE)
 FEATURES Location/Qualifiers
 source 1..25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="D0A1 Heterozygote Primer Sequence"
 BASE COUNT 3 a 2 c 2 g 18 t
 ORIGIN
 Query Match 0.4%; Score 20; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5202 AATCTAAAAAAAAAAAAA 5221
 ||||||||||||||||||
 Db 20 AATCTAAAAAAAAAAAAA 1
 ||||||||||||||||||
 RESULT 7
 DDICTINBA
 LOCUS DDICTINBA 91 bp DNA linear INV 17-NOV-1995
 DEFINITION Dictyostellium discoideum actin 8-1 gene, 3' UTR.
 ACCESSION M25215
 VERSION M25215.1 GI:1066510
 KEYWORDS actin.
 SOURCE Dictyostellium discoideum DNA.
 ORGANISM Dictyostellium discoideum
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
 1 (bases 1 to 91)
 REFERENCES McKewen, M., Hirth, K.P., Edwards, C. and Firtel, R.A.
 TITLE Examination of the regulation of the actin multigene family in
 Dictyostellium discoideum
 JOURNAL MEDLINE 82275208
 PUBMED 7051026
 COMMENT On Nov 21, 1995 this sequence version replaced gi:341298.
 FEATURES Location/Qualifiers
 source 1..91
 /organism="Dictyostellium discoideum"
 /db_xref="taxon:44689"
 BASE COUNT 70 a 2 c 2 g 17 t
 ORIGIN
 Query Match 0.4%; Score 20; DB 3; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5202 AATCTAAAAAAAAAAAAA 5221
 ||||||||||||||||||
 Db 42 AATCTAAAAAAAAAAAAA 61
 ||||||||||||||||||
 RESULT 8
 G73641 94 bp DNA linear STS 16-JUL-2002
 LOCUS G73641
 DEFINITION R2696F etiolated leaf tissue of rice Oryza sativa STS genomic clone
 R2696 sequencing direction=forward, sequence tagged site.
 ACCESSION G73641
 VERSION G73641.1 GI:19697236
 KEYWORDS STS.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriatroidae; Oryzaceae; Oryza.
 1 (bases 1 to 94)
 REFERENCES Ehnrich, D.K., Winter, M.D., Haardt, M., Goldberg, Y.P., Waka, S.O.,
 Ponton, A., Allen, S.J., de Antueno, R.J. and Knickle, L.C.
 TITLE Oryza sativa STS
 JOURNAL Unpublished (2002)
 COMMENT

Contact: Susan R. McCouch
 Cornell University
 Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
 Tel: 6072550420
 Fax: 6072556683
 Email: srm4@cornell.edu
 Primer A: M13 universal Forward GTAAACGACGCGCAGT
 Primer B: M13 universal Reverse AACGACATGACCATG
 STS size: 94
 Protocol:
 Template: 20-100ng
 Primer: 5pmol each
 DNTPs: 40umol
 Tag polymerase: 5units
 Total volume: 50ul
 Buffer:
 Tris-HCl: 100mM
 KCl: 50mM
 MgCl2: 15mM
 Gelatin: 0.1%
 PH: 8.3
 This is a partial sequence of the RFLP clone named above that was
 mapped at Cornell University Plant Breeding Dept. and sequenced at
 the Genome Sequencing Center at Cold Spring Harbor Laboratory. This
 marker is located on rice chromosome 3. For citations and other
 related information concerning this probe, please refer to the
 Gramene database at <http://www.Gramene.org>.
 FEATURES Location/Qualifiers
 source 1..94
 /organism="Oryza sativa"
 /cultivar="IR36"
 /db_xref="taxon:4530"
 /map="3"
 /clone="R2696"
 /clone_lib="etiolated leaf tissue of rice"
 /note="Vector: Lambda ZAP II/pBluescript; V-type: Plasmid;
 A lambda ZAP II cDNA library was constructed from mRNA
 extracted from etiolated leaf tissue of the rice cultivar
 'IR36' and converted to pBluescript (amp resistant) as
 described in Cause et al. (1994) Genetics 138:1251-1274.
 For insert amplification, use M13 forward and reverse
 primers. Restriction site is EcoRI. Clones from this
 library are designated with the prefix 'RZ..'
 <1..>94
 BASE COUNT 2 a 6 c 12 g 74 t
 ORIGIN
 STS
 Query Match 0.4%; Score 20; DB 11; Length 94;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4501 TTTT TTTT TTTT TTTT TTTT GGCTT 4520
 ||||||||||||||||||
 Db 52 TTTT TTTT TTTT TTTT TTTT GGCTT 71
 ||||||||||||||||||
 RESULT 9
 AX431447 28 bp DNA linear PAT 28-JUN-2002
 LOCUS AX431447/c
 DEFINITION Sequence 80 from Patent WO0240666.
 ACCESSION AX431447
 VERSION AX431447.1 GI:21656293
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct.
 artificial sequences.
 REFERENCES
 1 Ehnrich, D.K., Winter, M.D., Haardt, M., Goldberg, Y.P., Waka, S.O.,
 Ponton, A., Allen, S.J., de Antueno, R.J. and Knickle, L.C.
 TITLE Fat regulated genes, uses thereof, and compounds for modulating
 same

JOURNAL Patent: WO 0240666-A 80 23-MAY-2002;
XENON GENETICS INC (CA)
FEATURES Location/Qualifiers
Source 1..28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
BASE COUNT 6 a 7 c 8 g 7 t
ORIGIN

Query Match 0.4%; Score 19; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 206 GGAAGTATCCGCGATC 224
|||||
DB 28 GGAAGTATCCGCGATC 10

RESULT 10
AX484032 65 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 1332 from Patent WO02053728.
DEFINITION AX484032
ACCESSION AX484032
VERSION AX484032.1 GI:22318384
KEYWORDS
SOURCE
ORGANISM
Candida albicans.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Mitosporic Saccharomycetales; Candida.
REFERENCE
1 Roemer, T., Jiang, B., Boone, C., Bussey, H. and Olsen, K. L.
Gene disruption methodologies for drug target discovery
Patent: WO 02053728-A 1332 11-0UL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
Source 1..65
/organism="Candida albicans"
/db_xref="taxon:5476"
BASE COUNT 29 a 10 c 1 g 25 t
ORIGIN

Query Match 0.4%; Score 19; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2392 AATATATATATATATA 2410
|||||
DB 32 AATATATATATATATA 14

RESULT 11
E32451 18 bp DNA linear PAT 18-JUN-2001
LOCUS Mammal-derived tissue specific physiologically active protein.
ACCESSION E32451
DEFINITION E32451.1 GI:13018687
VERSION E32451.1 GI:13018687
KEYWORDS JP 2000037190-A/11.
SOURCE synthetic construct.
ORGANISM
synthetic construct.
REFERENCE
1 (bases 1 to 18)
Jun, N., Yusuke, N. and Toshihiro, T.
Mammal-derived tissue specific physiologically active protein
Patent: JP 2000037190-A 11 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT
OS Artificial Sequence
PN JP 2000037190-A/11
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC

C12N15/02,
PC C12P21/02, C12P21/08, (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FT Key Location/Qualifiers
PR primer_bind (1)..(18).
FEATURES
Source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 0 a 0 c 3 g 15 t
ORIGIN

Query Match 0.3%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4500 GTTTTGTGTTTGTG 4517
|||||
DB 1 GTTTTGTGTTTGTG 18

RESULT 12
AR051300 35 bp DNA linear PAT 29-SEP-1999
LOCUS AR051300
DEFINITION Sequence 17 from patent US 5830662.
ACCESSION AR051300
VERSION AR051300.1 GI:5974664
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 35)
Soares, M.B. and Estratidis, A.
Method for construction of normalized cDNA libraries
Patent: US 5830662-A 17 03-NOV-1998;
JOURNAL Location/Qualifiers
FEATURES
Source 1..35
/organism="unknown"
BASE COUNT 7 a 0 c 1 g 27 t
ORIGIN

Query Match 0.3%; Score 18; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4498 AAGTTTGTGTTTGT 4515
|||||
DB 16 AAGTTTGTGTTTGT 33

RESULT 13
I16948 35 bp DNA linear PAT 03-APR-1996
LOCUS I16948
DEFINITION Sequence 17 from patent US 5482845.
ACCESSION I16948
VERSION I16948.1 GI:1251856
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 35)
Soares, M.B. and Estratidis, A.
Method for construction of normalized cDNA libraries
Patent: US 5482845-A 17 09-JAN-1996;
JOURNAL Location/Qualifiers
FEATURES
Source 1..35
/organism="unknown"
BASE COUNT 7 a 0 c 1 g 27 t
ORIGIN

Query Match 0.3%; Score 18; DB 6; Length 35;

Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4498 AACGTTTTTTTTTTTTTT 4515

Db 16 AACGTTTTTTTTTTTTTT 33

RESULT 14

LOCUS 145742 35 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 17 from patent US 5637685.

ACCESSION 145742

VERSION 145742.1 GI:2469844

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 35)

AUTHORS Soares, M.B. and Estratiadis, A.

TITLE Normalized cDNA libraries

JOURNAL Patent: US 5637685-A 17 10-JUN-1997;

FEATURES Location/Qualifiers

source 1..35

BASE COUNT 7 a 0 c 1 g 27 t

ORIGIN

Query Match 0.38; Score 18; DB 6; Length 35;

Best Local Similarity 100.0%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;

OY 4498 AACGTTTTTTTTTTTTTT 4515

Db 16 AACGTTTTTTTTTTTTTT 33

RESULT 15

LOCUS AR184440 42 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 8 from patent US 6346384.

ACCESSION AR184440

VERSION AR184440.1 GI:20230405

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 42)

AUTHORS Poliner, R.B.

TITLE Real-time monitoring of PCR using LOCI

JOURNAL Patent: US 6346384-A 8 12-FEB-2002;

FEATURES Location/Qualifiers

source 1..42

BASE COUNT 4 a 6 c 4 g 28 t

ORIGIN

Query Match 0.3%; Score 18; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.9e+03; Mismatches 0; Indels 0; Gaps 0;

OY 5204 TCTAAAAAAAAAAAAA 5221

Db 23 TCTAAAAAAAAAAAAA 6

Search completed: November 14, 2002, 05:50:56
Job time : 8697 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2002, 18:48:56 : Search time 115 Seconds
(without alignments)
13923.125 Million cell updates/sec

Title: US-09-918-187-3

Perfect score: 5221
Sequence: 1 ataaaaggggctgaggaagaa.....aactctaaaaaataaaaaa 5221

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 684418

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	0.7	33	1	US-08-332-420-62
2	21	0.4	95	1	US-08-518-878B-3
3	21	0.4	95	1	US-08-294-522B-3
4	21	0.4	95	2	US-08-807-861A-3
5	21	0.4	95	2	US-08-470-868A-3
6	21	0.4	95	3	US-09-210-681-3
7	21	0.4	95	3	US-08-946-719A-3
8	18	0.3	23	5	PCT-US94-05407-8
9	18	0.3	33	5	PCT-US94-05407-7
10	18	0.3	33	1	US-09-187-355-1
11	18	0.3	35	1	US-08-126-594-17
12	18	0.3	35	1	US-08-465-811A-17
13	18	0.3	35	2	US-08-618-542B-17
14	18	0.3	38	2	US-08-771-624B-21
15	18	0.3	39	4	US-09-619-103-4
16	18	0.3	42	4	US-09-536-936-8
17	18	0.3	46	1	US-07-915-245-3
18	18	0.3	46	5	PCT-US94-05407-3
19	18	0.3	46	5	PCT-US94-05407-10
20	18	0.3	68	3	US-09-052-924-1
21	17	0.3	20	1	US-07-912-900-20
22	17	0.3	20	1	US-08-285-309-20
23	17	0.3	20	1	US-08-313-075A-11
24	17	0.3	20	3	US-08-502-046-20
25	17	0.3	20	3	US-09-120-853-4
26	17	0.3	20	4	US-09-228-942-7
27	17	0.3	20	4	US-08-482-918-32

c 28	17	0.3	20	4	US-08-482-918-33	Sequence 33, Appl
c 29	17	0.3	20	4	US-09-224-681-32	Sequence 32, Appl
c 30	17	0.3	20	4	US-09-224-681-33	Sequence 33, Appl
c 31	17	0.3	20	4	US-08-336-728A-32	Sequence 32, Appl
c 32	17	0.3	20	4	US-08-336-728A-33	Sequence 32, Appl
c 33	17	0.3	23	1	US-08-018-129-15	Sequence 15, Appl
c 34	17	0.3	23	1	US-08-621-914A-6	Sequence 6, Appl
c 35	17	0.3	23	2	US-08-448-250-15	Sequence 15, Appl
c 36	17	0.3	23	3	US-09-056-052-9	Sequence 9, Appl
c 37	17	0.3	24	4	US-08-906-156A-82	Sequence 82, Appl
c 38	17	0.3	26	1	US-08-014-943A-21	Sequence 21, Appl
c 39	17	0.3	26	1	US-08-486-421-15	Sequence 15, Appl
c 40	17	0.3	26	1	US-08-470-911-15	Sequence 15, Appl
c 41	17	0.3	26	2	US-08-486-809-15	Sequence 15, Appl
c 42	17	0.3	26	4	US-09-475-316A-59	Sequence 59, Appl
c 43	17	0.3	30	1	US-08-181-271A-85	Sequence 85, Appl
c 44	17	0.3	30	1	US-08-158-189-43	Sequence 43, Appl
c 45	17	0.3	30	1	US-08-449-315-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-332-420-62
Sequence 62, Application US/08332420
Patent No. 5744300
GENERAL INFORMATION:
APPLICANT: Maarten H.K. Linskens, et al.
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE
TITLE OF INVENTION: IDENTIFICATION AND REGULATION
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,420
FILING DATE: October 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,180
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 39
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-332-420-62
Query Match 0.7%; Score 39; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1412 AGATGATGATGTAAACCATTCACATGACATGATTCCTTT 1450

Db 1 AGATGATGATGTTAAACCATTCAGTACAGTATCTTT 39

RESULT 2

US-08-518-878B-3
Sequence 3, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-518-878B-3
Query Match 0.4%; Score 21; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5069 TTTTCCCTTTTATGTGGG 5089
Db 74 TTTTCCCTTTTATGTGGG 94

US-08-294-522B-3
Sequence 3, Application US/08294522B
Patent No. 5741666

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,522B
FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-294-522B-3

Query Match 0.4%; Score 21; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5069 TTTTCCCTTTTATGTGGG 5089
Db 74 TTTTCCCTTTTATGTGGG 94

US-08-807-861A-3
Sequence 3, Application US/08807861A
Patent No. 5853975

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-807-861A-3

Query Match 0.4%; Score 21; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
|||||
DB 74 TTTTTCCTTTTATGTGGG 94

RESULT 5
US-08-470-868A-3
Sequence 3, Application US/08470868A
Patent No. 5861485

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864

TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-3

Query Match 0.4%; Score 21; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
|||||
DB 74 TTTTTCCTTTTATGTGGG 94

RESULT 6
US-09-210-681-3
Sequence 3, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-210-681-3

Query Match 0.4%; Score 21; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTGGG 5089
|||||
DB 74 TTTTTCCTTTTATGTGGG 94

RESULT 7
US-08-946-719A-3
Sequence 3, Application US/08946719A
Patent No. 6121017

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,719A
; FILING DATE: 8-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/807,861
; FILING DATE: 26-FEB-1997
; APPLICATION NUMBER: US 08/518,878
; FILING DATE: 23-AUG-1995
; APPLICATION NUMBER: US 08/470,868
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/294,522
; FILING DATE: 23-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-946-719A-3

Query Match          0.4%; Score 21; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5069 TTTTTCCTTTTATGTCGG 5089
      |||||||
DB 74 TTTTTCCTTTTATGTCGG 94

RESULT 8
PCT-US94-05407-7/C
; Sequence 7, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
;
PCT-US94-05407-7

Query Match          0.3%; Score 18; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-187-355-1
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4501 TTTTTCCTTTTATGTCGG 4518
      |||||||
DB 20 TTTTTCCTTTTATGTCGG 3

RESULT 9
PCT-US94-05407-8
; Sequence 8, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
;
PCT-US94-05407-8

Query Match          0.3%; Score 18; DB 5; Length 23;
Best Local Similarity 16.7%; Pred. No. 7.8e+02;
Matches 3; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 4501 TTTTTCCTTTTATGTCGG 4518
      |||||||
DB 4 UUUUUUUUUUUUUUUUUUU 21

RESULT 10
US-09-187-355-1
; Sequence 1, Application US/09187355B
; Patent No. 6118126
; GENERAL INFORMATION:
; APPLICANT: Sarnoff Corporation
; APPLICANT: Zanzucchi, Peter F.
; TITLE OF INVENTION: Method for Enhancing Fluorescence
; FILE REFERENCE: SAR-12215A
; CURRENT APPLICATION NUMBER: US/09/187,355B
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 08/961,860
; EARLIER FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown Organism
;
US-09-187-355-1

Query Match          0.3%; Score 18; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AACGTTTTTTTTTTTTT 4515
|||||

DB 15 AAGTTTTTTTTTTTTT 32

RESULT 11

US-08-126-594-17
Sequence 17, Application US/08126594

Patent No. 5482845

GENERAL INFORMATION:

APPLICANT: Soares, M. Bento

TITLE OF INVENTION: Eftstraliadis, Argiris

TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/126.594

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPW/AKC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-126-594-17

Query Match

Best Local Similarity 100.0%; Score 18; DB 1; Length 35;
Pred. No. 7.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AACGTTTTTTTTTTTTT 4515
|||||

DB 16 AAGTTTTTTTTTTTTT 33

RESULT 12

US-08-465-811A-17

Sequence 17, Application US/08465811A

Patent No. 5637685

GENERAL INFORMATION:

APPLICANT: Soares, M. Bento

TITLE OF INVENTION: Eftstraliadis, Argiris

TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465.811A

FILING DATE: June 6, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPW/AKC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-465-811A-17

Query Match

Best Local Similarity 100.0%; Score 18; DB 1; Length 35;
Pred. No. 7.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AACGTTTTTTTTTTTTT 4515
|||||

DB 16 AAGTTTTTTTTTTTTT 33

RESULT 13

US-08-619-542B-17

Sequence 17, Application US/08619542B

Patent No. 5630662

GENERAL INFORMATION:

APPLICANT: The Trustees of Columbia University in the City

TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/619.542B

FILING DATE: June 21, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840-A-PCT-US

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-619-542B-17

Query Match
Best Local Similarity 100.0%; Score 18; DB 2; Length 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AAGTTTTTTTTTTTTTTT 4515
Db 16 AAGTTTTTTTTTTTTTTT 33

RESULT 14
US-08-771-624B-21
Sequence 21, Application US/08771624B
Patent No. 5914230
GENERAL INFORMATION:
APPLICANT: Liu, Yen Ping
APPLICANT: Patel, Rajesh D.
APPLICANT: Kurn, Nurich
APPLICANT: Liu, Claire
APPLICANT: Rose, Samuel J.
APPLICANT: Ullman, Edwin F.
TITLE OF INVENTION: Homogeneous Amplification and Detection
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Behring Diagnostics GmbH, c/o Dade Behring Inc.
STREET: 1717 Deerfield Road
CITY: Deerfield
STATE: Illinois
COUNTRY: US
ZIP: 60015-0778
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,624B
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,090
FILING DATE: 22-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ruszala, Lois K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: 1030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 267-5364
TELEFAX: (847) 267-6024
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-08-771-624B-21

Query Match
Best Local Similarity 100.0%; Score 18; DB 2; Length 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4498 AAGTTTTTTTTTTTTTTT 4515
Db 16 AAGTTTTTTTTTTTTTTT 33

RESULT 15
US-09-619-103-4
Sequence 4, Application US/09619103
Patent No. 6429300
GENERAL INFORMATION:
APPLICANT: Kurz, Markus
APPLICANT: Lohse, Peter
APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/09/619,103
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: designed sequence to act as a linker
US-09-619-103-4

Query Match
Best Local Similarity 100.0%; Score 18; DB 4; Length 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5204 TCTAAAAAAAAAAAAA 5221
Db 8 TCTAAAAAAAAAAAAA 25
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Search completed: November 14, 2002, 01:16:48
Job time : 119 secs